

**GENETICAL STUDIES ON NO₃⁻ USE EFFICIENCY UNDER
AEROBIC AND ANAEROBIC CONDITIONS
IN RICE (*Oryza sativa* L.)**

Ph.D. Thesis

By

Ambhure Ram Ganpatrao

**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
FACULTY OF AGRICULTURE
INDIRA GANDHI KRISHI VISHWAVIDYALAYA,
RAIPUR (CHHATTISGARH)**

2017

**GENETICAL STUDIES ON NO₃⁻ USE EFFICIENCY UNDER
AEROBIC AND ANAEROBIC CONDITIONS
IN RICE (*Oryza sativa* L.)**

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur

By

Ambhure Ram Ganpatrao

**IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE DEGREE OF**

Doctor of Philosophy

In

Agriculture

(Genetics and Plant Breeding)

Roll No. 20141520530

ID No. 130114027

JULY, 2017

CERTIFICATE - I

This is to certify that the thesis entitled "**Genetical studies on NO_3^- use efficiency under aerobic and anaerobic conditions in rice (*Oryza sativa* L.)**" submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy in Agriculture** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), is a record of the bonafide research work carried out by **Ambhure Ram Ganpatrao** under my/our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by him.

Date: 19.7.17


Chairman

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

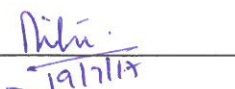
Chairman (Dr. A. K. Sarawgi)



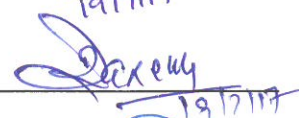
Member (Dr. S. B. Verulkar)



Member (Dr. Ritu R. Saxena)


19/7/17

Member (Dr. Ravi R. Saxena)

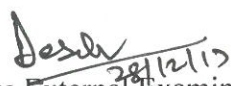

19/7/17

Member (Dr. A.K. Sarawgi)



CERTIFICATE - II

This is to certify that the thesis entitled "**Genetical studies on NO_3^- use efficiency under aerobic and anaerobic conditions in rice (*Oryza sativa* L.)**" submitted by **Ambhure Ram Ganpatrao** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfilment of the requirements for the degree of **Doctor of Philosophy in Agriculture** in the Department of **Genetics and Plant Breeding** has been approved by the external examiner and Student's Advisory Committee after oral examination.


Signature External Examiner
(Name: **D.B. Deosarkar**)

Date: **28.12.17**

Major Advisor


28.12.17

Head of the Department


28.12.17

Faculty Dean

Approved/Not approved

Director of Instructions

ACKNOWLEDGEMENT

First of all, I praise God SHIVA and GANESHA, the almighty, merciful and passionate, for providing me this opportunity and granting me the capability to proceed successfully.

At the very outset, I express my deepest sense of gratitude to Dr. A. K. Sarawgi, Professor and Head, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, the erudite chairman of my advisory committee for suggesting, the research problem and for his constant, immaculate, indefatigable guidance, affectionate treatment, constructive criticism, painstaking efforts taken for scrutinizing the manuscript and encouragement during the final shaping of this thesis. Words would be a poor vehicle to communicate him my deepest sense of gratitude.

I would like to express my deep sense of gratitude and great indebtedness to my advisory committee, Dr. S. B. Verulkar, Professor and Head, Department of Plant Molecular Biology and Biotechnology. Dr. Ritu R. Saxena, Asso. Professor, Department of Genetics and Plant Breeding and Dr. Ravi R. Raxena, Professor, Department of Agriculture Statistics and Social Science, whose valuable worthy suggestions and timely guidance helped me to put the dissertation in present form.

I would like to place my sincere thanks to my beloved teachers Dr. Deepak Sharma, Dr. Sandeep Bhandarkar, Dr. Sunil Nair, Dr. Bhawana Sharma, Dr. Prabharani Choudary and Smt. Mangala Parikh, Department of genetics and Plant Breeding, for their kind help during the course and their guidance throughout my academic and research investigation. I also express my sincere thanks to Dr. Sanjeeva Rao, Scientist, IIRR (former DRR), Hyderabad for his valuable corporation during research work.

I wish to record my sincere thanks to Dr. S. K. Patil, Hon'ble Vice Chancellor, Dr. S. S. Rao, Director of Research Services, Dr. S. S. Shaw, Director of Instructions, IGKV, Dr. O. P. Kashyap, Dean, Dr. (Major) G. K. Shrivastva, Dean of Student welfare, College of Agriculture, IGKV, and Mr. S. R. Verma, Registrar, IGKV, Raipur for providing me the necessary facilities for research work.

Sincerest thanks are also extending to the all scientists of Department of Genetics and Plant Breeding, COA, Raipur, for their academic, technical and logistic help.

I would like to express my sincere gratitude to Dr. Madhav Pandey (Librarian, Nehru Library, Raipur) and Shri U.K. Watti for giving me their kind help during my study.

I think, having true and caring senior is one of the greatest achievements of one's life. I am bit luckier than anybody else in having loving and intimate senior like Dr. Hemant and Dr. Rashmi, without whom I would never have got my academic and research achievements. I would also express thanks to Dr. Satyapaal, Mr. Ojha, Dr. Namrata, Dr. Mangesh, Dr. Ransing, Dr. Ravi, Dr. Narendra and my friends Gajanan, Satyajeeet, Shantikumar, Laxman, Anand for their unrelenting help and support and for keeping my moral high.

I express my deepest thanks to my batchmates Parmeshwar, Umesh, Naveen, Ishu, Priti, Vishwajeet, Roshan, Anurag, Devidas and Juniors; Abhishek, Harsh, Ravi Raj, Roshan, Sopan, Suman, Rajendra for their kind support and encouragement.

I am also thankful to Mr. Bhedi Bhaiya, Mr. Badku uncle, Manish Bhaiya and Moti Bhaiya, for helping me throughout my research work.

Everything in my life is nothing without the selfless care, boundless love and treatment moral support of the member of my family. No words are enough to express the greatest sacrifice, devotion and constant encouragement of my respected and adorable father Shri. Ganpatrao Kishanrao Ambhure, mother Sau. Sarswathi Ganpatrao Ambhure, my brothers Shrihari, Krishna, my sisters Varsha, Deepali and brother-in-law Shri. Manik Deshmukh and Shri. Mithun Deshmukh.

Last but never the least, it is difficult to list all those whom I express my gratitude for their goodwill and moral support during my academic attainment though nobody is mentioned none is forgotten too..... Thanks for all your encouragement!

Department of Genetics and Plant Breeding
College of Agriculture
IGKV, Raipur (C.G.)
Date: 18-07-2017

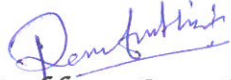

Ambhure Ram G.

TABLE OF CONTENTS

Chapter	Title	Page
	ACKNOWLEDGEMENT	iii
	TABLE OF CONTENTS	v
	LIST OF TABLES	vii
	LIST OF FIGURES	x
	LIST OF NOTATIONS	xi
	LIST OF ABBREVIATIONS	xii
	ABSTRACT	xiv
I	INTRODUCTION	1
II	REVIEW OF LITERATURE	5
	2.1 Water Deficit and their impact on grain yield and nitrogen Use Efficiency	5
	2.2 Genetic Variability of grain yield and improving NUE	8
	2.3 Association studies in relation to grain yield and nitrogen use efficiency	15
	2.4 Heritability	20
	2.5 Root characteristics	23
	2.6 Assessment of stability for grain yield	25
	2.7 Quality Parameters	26
	2.8 Molecular markers and diversity analysis	33
	2.9 Identification of quantitative trait loci for grain yield and its components	35
III	MATERIALS AND METHODS	39
	3.1 Experimental site	39
	3.2 Physio-chemical characteristics of soil of the experimental field	39
	3.3 Climatic and weather conditions	39
	3.4 Materials	41
	3.5 Experimental details	42
	3.6 Sowing and Cultural practices	43
	3.7 Observations recorded under field conditions	45
	3.8 Nitrogen estimation	50
	3.9 Assessing effect of NH_4^+ -N and NO_3^- -N treatment on root growth under soil-filled glass rhizotrons	53
	3.10 Molecular studies	57
	3.11 Preparation of Buffers and chemicals	60
	3.12 Statistical analysis	63

3.12.1	Analysis of variance	63
3.12.2	Parameters of variation	64
3.12.3	Estimation of Variability	66
3.12.4	Heritability (broad sense)	66
3.12.5	Estimation of Genetic Advance as percentage of mean	67
3.12.6	Character association	67
3.12.7	Cluster analysis	68
3.12.8	Stability analysis	69
3.13	QTL analysis	69
IV	RESULTS AND DISCUSSION	70
4.1	Analysis of Variance for augmented design	71
4.2	Analysis of variance for factorial design	82
4.3	Variability studies	95
4.4	Association study	101
4.5	Root traits study under different nitrogen regimes	112
4.6	Stability analysis	119
4.7	Quality study	123
4.8	Molecular diversity analysis	140
4.9	Single marker analysis	144
V	SUMMARY AND CONCLUSIONS	150
	REFERENCES	156
	APPENDICES	183
	Appendix A	183
	Appendix B	184
	Appendix C	185
	Appendix D	187
	Appendix E	189
	Appendix F	192
	Appendix G	195
	Appendix H	198
	Appendix I	200
	Appendix J	207
	Appendix K	209
	Appendix L	211
	RESUME	212

LIST OF TABLES

Table	Title	Page
3.1	Physio-chemical properties of the soil from the experimental field	40
3.2	List of genotypes used under study	41
3.3	Characteristic features of parent of RILs	42
3.4	Treatments for studying NH_4^+ and NO_3^- use efficiency wet season 2016	43
3.5	General information about sowing	43
3.6	Observations recorded after Root scanning using WinRhizo software	57
3.7	PCR mix for one reaction (Volume 10 μl)	59
3.8	Temperature profile used for PCR amplification using microsatellite markers	59
3.9	Scoring SSR banding pattern in RILs population	60
3.10	Skeleton of ANOVA table for augmented design	64
3.11	Skeleton of ANOVA table for factorial design	65
4.1	ANOVA for yield and yield contributing traits under N^0 , NO_3^- and NH_4^+ form of nitrogen and variable environments during wet season-2015	73
4.2	Mean phenotypic performance, range and their respective germplasm accession name for yield and yield contributing traits under different N regimes and environments during wet season-2015	75
4.3	Mean phenotypic performance, range with respective line Number, standard deviation, standard error of RILs population for yield and yield contributing traits under different N regimes for aerobic condition during wet season-2015	79
4.4	List of selected genotypes based on grain yield under different nitrogen regimes for aerobic conditions along with their ranking during wet season 2015	81
4.5	Top ten lines among 32 selected RILs based on grain yield under different nitrogen regimes for aerobic conditions during wet season 2015	82
4.6	Analysis of variance for comparison of 38 selected germplasm accessions under N^0 , NO_3^- and NH_4^+ forms of nitrogen and variable environments for yield and yield related traits during wet season, 2016	83

4.7	Analysis of variance for comparison of 38 selected germplasm accessions under N^0 , NO_3^- and NH_4^+ forms of nitrogen and variable environments for NUE and its related traits during wet season, 2016	84
4.8	Mean phenotypic performance, genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance for yield and yield related traits of germplasm accessions under differential N regimes and environments during wet season, 2016	93
4.9	Mean phenotypic performance, genotypic and phenotypic coefficient of variation, heritability and genetic advance for NUE and its related traits of germplasm accessions under differential N regimes and environments during wet season, 2016	94
4.10.1	Genotypic correlation between grain yield and NUE traits for N^0 under aerobic and anaerobic condition	104
4.10.2	Genotypic correlation between grain yield and NUE traits for NO_3^- under aerobic and anaerobic condition	105
4.10.3	Genotypic correlation between grain yield and NUE traits for NH_4^+ under aerobic and anaerobic condition	106
4.11.1	Direct and Indirect effect of yield contributing and NUE traits upon grain yield for N^0 under aerobic and anaerobic conditions	109
4.11.2	Direct and indirect effect of yield contributing and NUE traits upon grain yield for NO_3^- under aerobic and anaerobic conditions	110
4.11.3	Direct and indirect effect of yield contributing and NUE traits upon grain yield for NH_4^+ under aerobic and anaerobic conditions	111
4.12	Genotypic differences for root and shoot traits among selected rice genotypes grown under mini-rhizotron (12 genotypes)	114
4.13	Correlation, direct and indirect effect of root traits over grain yield under three N regimes	118
4.14	Pooled analysis of variance and stability parameters for grain yield for different N regimes and variable environments during wet season 2016	120
4.15	Estimate of different stability parameters for grain yield for aerobic and anaerobic condition during wet season 2016	122
4.16	Correlation of 12 quality traits of 38 selected rice accession under aerobic and anaerobic condition	130
4.17.1	Clustering pattern of 38 rice genotypes based on D^2 analysis for aerobic condition	132
4.17.2	Clustering pattern of 38 rice genotypes based on D^2 analysis for anaerobic condition	132

4.18	Average intra (diagonal) and inter cluster distances for quality traits	133
4.19	Cluster mean values for different quality traits under aerobic and anaerobic condition	135
4.20.1	Mean value of iron and zinc content under variable N regimes and environment	139
4.20.2	Top lines with high Zn Content in rice under aerobic condition	139
4.20.3	Top lines with high Zn Content in rice under anaerobic condition	139
4.21	Details of primers used for developing genotypic data for 38 germplasm accessions	141
4.22	Details of primers used for developing genotypic data for 32 RILs population	146
4.23	The t-test analysis of primers for grain yield and yield contributing traits	148

LIST OF FIGURE

Figure	Title	Page
3.1(a)	Maximum, minimum temperature and rainfall during the field evaluation of study material (wet season 2015)	40
3.1 (b)	Maximum, minimum temperature and rainfall during the field evaluation of study material (wet season 2016)	40
3.2	General view of field experiment under $\text{NO}_3^- \text{N}$ and $\text{NH}_4^+ \text{N}$ treatment for aerobic condition during wet season -2015	44
3.3	General view of field experiment under $\text{NO}_3^- \text{N}$ and $\text{NH}_4^+ \text{N}$ treatment for aerobic condition during wet season -2016	44
3.4	A set of selected lines grown in thin glass rhizotrons	53
4.1	Variability and Morphological differences of root under N^0 , NO_3^- and NH_4^+ condition	115
4.2	PCR amplification of 38 germplasm accessions of rice with SSR primer RM-1233, RM-242, RM-316 and HvSSR-10-01	143
4.3	UPGMA-based molecular dendogram of SSR and HvSSR markers showing 38 rice germplasm	144
4.4	Banding pattern of RM-18655, RM-1233, RM-18616, RM-18620, HvSSR-9-37 and RM-408	147

LIST OF NOTATIONS/SYMBOLS

%	Per cent
°C	Degree Celsius
μl	Microlitre
bp	Base pairs
cm	Centimeter
cM	Centimorgan
d.f.	Degree of freedom
<i>et al.</i>	And Others
g	Gram
gg ⁻¹ N	Gram per gram nitrogen
H ₂ O	Water
ha	Hectare
HCl	Hydrochloric Acid
hrs	Hours
<i>i.e.</i>	That is
KCl	Potassium chloride
m	Meter
M	Molar
mb	Megabase Pairs (10 ⁶ bp)
MgCl ₂	Magnesium Chloride
min	Minutes
ml	Milliliter
NaCl	Sodium Chloride
ng	Nanogram
rpm	Rotations Per Minute
U	Units

LIST OF ABBREVIATION

100SW	100 Seed Weight
Approx.	Approximately
ARD	Average Root Diameter
BNY	Biomass Nitrogen Yield
BT	Basmati Type
BY	Biological yield
CCSD	Chlorophyll Content at Seedling Stage
CCFW	Chlorophyll Content at Flowering Stage
Chr	Chromosome
cm	Centimeter
dATP	Deoxy adenosine 5' triphosphate
dCTP	Deoxy cytidine 5' triphosphate
dGTP	Deoxy guanosine 5' triphosphate
DNA	Deoxyribo nucleic acid
dNTPs	Deoxynucleotide triphosphates
DF	Days to 50% Flowering
dTTP	Deoxy thymidine 5' triphosphate
EDTA	Ethylene Diamine Tetra Acetic Acid
ER	Elongation Ratio
EI	Elongation Index
EtOH	Ethanol
EtBr	Ethidium Bromide
ET	Effective Tillers per Plant
GNC	Grain Nitrogen Content
GNY	Grain Nitrogen Yield
GPC	Grain Protein Content
GS	Grain Shape
GY	Grain Yield
H	Hulling
HI	Harvest Index
HRR	Head Rice Recovery
KB	Kernel Breadth
KBAC	Kernel Breadth After Cooking
KL	Kernel Length
KLAC	Kernel Length After Cooking
LB	Long Bold

L:B	Length: Breadth Ratio
LLI	Length of Last Internode
LRD	Lateral Root Development
LS	Long Slender
M	Milling
MAS	Marker Assisted Selection
MS	Medium Slender
NILs	Near Isogenic Lines
NHI	Nitrogen Harvest Index
SPP	Number of Spikelet per Panicle
FGP	Number of Filled Grains per panicle
NU _p E	Nitrogen Uptake Efficiency
NU _t E	Nitrogen Utilization Efficiency
NUE	Nitrogen Use Efficiency
PCR	Polymerase Chain Reaction
PHSD	Plant Height at Seedling
PHMT	Plant Height at Maturity
PL	Panicle Length
QTL	Quantitative Trait Loci
RCBD	Randomized Complete Block Design
RIL	Recombinant Inbred Line
RL	Root Length
RV	Root Volume
SB	Short Bold
SDS	Sodium Dodecyl Sulphate
SH	Seedling Height
SLL	Second Leaf Length
SLW	Second Leaf Width
SF	Spikelet Fertility
SNC	Straw Nitrogen Content
SNY	Straw Nitrogen Yield
SSR	Simple Sequence Repeats
TBE	Tris Boric Acid EDTA buffer
TEMED	N,N,N',N'-Tetram Ethylethylene Di Amine
TW	Test weight
WU	Water Uptake

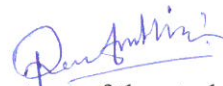
THESIS ABSTRACT

- a) Title of Thesis : Genetical studies on NO_3^- use efficiency under aerobic and anaerobic conditions in rice (*Oryza sativa* L.)
- b) Full Name of Student : Ambhure Ram Ganpatrao
- c) Major Subject : Genetics and Plant Breeding
- d) Name and Address of the major Advisor : Dr. A. K. Sarawgi
Professor and Head, Department of Genetics and Plant Breeding, CoA, IGKV, Raipur (C.G.), 492012
- e) Degree to be Awarded : Ph. D. (Agriculture)

Signature of Major Advisor

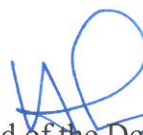


Signature of the student



Date: 19.7.17

Signature of Head of the Department



19.7.17

ABSTRACT

Rice (*Oryza sativa* L.) is the world's largest cultivated food crop and a main staple food for more than 50% of the world population. Faced with scarcity of water resources, soil moisture stress becomes most critical threat to rice production. Limited water that reduces nutrient availability to the plant. Presently water scarcity have been chased and breeders even developed a new plant type "aerobic rice" targeted at water limited rice environment but nutrient stress as a major constraints in most rice-based aerobic system in Asia. Among essential plant nutrients, nitrogen (N) is one of the most yield limiting nutrients for upland rice production. Nitrogen fertilizer applied in the form of urea as it is the main nitrogen carrier worldwide in annual crop production. Plant-useable N is consumed as nitrate (NO_3^-) from aerobic soils and as ammonium (NH_4^+) from flooded wetland, anaerobic soil. The current average nitrogen use efficiency (NUE) in the rice field is approximately 33%, poorest among cereals and a substantial proportion of the remaining 67% is lost into the environment. The complex nature of nitrogen fertilizer response particularly in the form of nitrate in aerobic soil, inefficient

phenotypic selection and difficulty of effective low nitrogen tolerance screening methodology complicate the development of nitrogen responsive varieties. Therefore, the present study was undertaken to carry out the genetic analysis coupled with to identify efficient rice genotypes in response to grain yield and nitrogen use efficiency (in the form of nitrate) under aerobic cultivation.

123 rice lines including released varieties, advanced breeding lines, land races and checks were evaluated in augmented design with three treatment i.e. zero nitrogen, nitrogen in the form of calcium nitrate (NO_3^-) and nitrogen in the form of ammonium chloride (NH_4^+) with ratio of 80:60:40 NPK kg ha⁻¹ under aerobic and anaerobic condition during wet season 2015, at Department of Genetics and Plant Breeding Research Cum Instructional Farm, IGKV, Raipur, to generate the phenotypic data. On the basis of grain yield and other important ancillary traits, 38 lines were selected and evaluated by using three way factorial designs with three treatments and two replication under both aerobic and anaerobic conditions during wet season, 2016. The genetic parameters studied namely, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance, association, path coefficient and stability analysis.

Three way analyses revealed significant differences among the genotypes for all the traits indicating the presence of sufficient amount of genetic variation among genotypes and possibility of manipulating these variations for rice improvement. The genotype by nitrogen (G×N) interaction component was found significant for all traits under study. The trend analysis of NH_4^+ and NO_3^- dynamics revealed that NH_4^+ concentration persisted more under anaerobic condition and NO_3^- -N concentration under aerobic conditions. Mean performance of genotypes depicted higher values for agronomically important traits i.e. yield and NUE under NH_4^+ treatment as compared to NO_3^- and N^0 treatment under all environments.

In aerobic condition highest grain yield and nitrogen use efficiency was reported by RP 5125-2-4 of 244.35, 278.82 and 310.76g/m² under N^0 , NO_3^- and NH_4^+ respectively followed by IR-64 Drought (227.11, 268.17 and 300.62 g/m²) and RAU 1484-Aer-04 (200.75, 241.31 and 262.60 g/m²). This genotype gave stable performance

under different form of nitrogen for both aerobic and anaerobic condition. RCPR 8, CR 3634-1-3 and RP 5125-2-4 were reported highest grain nitrogen and protein content under N^0 , NO_3^- and NH_4^+ for aerobic condition. Phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters studied indicates that the apparent variation is not due to genotype but also due to the influence of environment.

High genetic advance coupled with high heritability was reported for plant height, biological yield, harvest index, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency and nitrogen utilization efficiency under differential N regimes and environments. This indicated that these traits were predominantly controlled by additive gene action and more amenable for selection. These traits were exhibit positive correlation along as well as showed direct effect on grain yield it reveals true relationship between them and direct selection for these traits will be rewarding for yield and NUE improvement. The genotype CR Dhan 40 contains consistently stable Zn content (in brown and polished rice grain) under different nitrogen regimes for both aerobic and anaerobic environments.

In another set 32 out of 179 RILs (between Swarna x Basmati-370) were selected on the basis of grain yield. These 32 lines along with their parent are used for further single marker analysis. Result revealed that, 5 QTLs have been identified for the trait plant height at maturity, of which 3 minor genes on chromosome # 5 and 1 each minor gene on chromosome # 8 and # 9. The 4 QTLs have been identified for chlorophyll content at seedling stage. Two QTLs on chromosome # 1 and # 5 have been identified for grain yield. RM-18616 on chromosome # 5 was found significantly linked with grain yield under all nitrogen regimes for aerobic condition.

These results assist us to identify NH_4^+ and NO_3^- responsive cultivars which could be used for cultivation and/or used as parent's in future breeding program to produce better nitrogen use efficiency varieties under aerobic and anaerobic conditions.

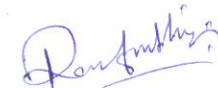
शोध सारांश

- अ) शोध का शीर्षक : धान (ओराइजा सटाइवा एल.) की एरोबिक और एनारोबिक स्थितियों में NO_3^- की उपयोग दक्षता पर आनुवंशिक अध्ययन।
- ब) छात्र का पूरा नाम : अंभुरे राम गणपतराव
- स) प्रमुख विषय : आनुवंशिकी एवं पादप प्रजनन
- द) प्रमुख सलाहकार का नाम एवं पता : डॉ. ए. के. सरावगि
प्राध्यापक एवं विभागाध्यक्ष,
आनुवंशिकी एवं पादप प्रजनन विभाग, कृषि महाविद्यालय,
इं. गा. कृ. वि., रायपुर (छ.ग.), 492012
- इ) डिग्री से सम्मानित किया जाना है : पी. एच. डी. (कृषि)

प्रमुख सलाहकार के हस्ताक्षर



दिनांक: 19.7.17


छात्र के हस्ताक्षर


विभागाध्यक्ष के हस्ताक्षर 19.7.17

सारांश

धान (ओराइजा सटाइवा एल.) विश्व की सबसे ज्यादा उगाई जाने वाली फसल है और विश्व की 50 प्रतिशत जन संख्या का प्रमुख खाद्य है। जल संसाधनों की कमी और मृदा नमी तनाव के कारण धान उत्पादन के लिए सबसे महत्वपूर्ण समस्या बन रही है। मृदा नमी तनाव तथा सीमित पानी पौधों की पोषक तत्व की उपलब्धता को कम करता है। वर्तमान में पानी की कमी का विचार विमर्श और अध्ययन करते हुए सीमित पानी के लिए प्रजनकों के द्वारा एरोबिक धान विकसित किया जा रहा है। जो की पानी सीमित धान के पर्यावरण पर परिलक्षित किया गया है, लेकिन एशिया में ज्यादातर धान आधारित एरोबिक स्थितियों में पोषक तत्वों की कमी प्रमुख बाधाओं के रूप में होती है। पौधे के आवश्यक पोषक तत्वों में नत्रजन (N), जो की उच्च भूमि में उगाए जाने वाली धान के लिए सबसे अहम पोषक तत्वों में से एक है। धान की वार्षिक फसल उत्पादन में विश्वभर में मुख्यरूप से नत्रजन उर्वरक यूरिया के रूप में दिया जाता है, क्योंकि यह एक मुख्य नत्रजन वाहक स्रोत है। नत्रजन धारण करने हेतु पौधा नत्रजन को एरोबिक स्थितियों में से नाइट्रेट (NO_3^-) और एनारोबिक स्थितियों में से अमोनियम (NH_4^+) के रूप में उपयोग करता है। धान के क्षेत्र में मौजूदा औसत नत्रजन उपयोग दक्षता (NUE) लगभग 33 प्रतिशत है, जो की अनाजवाली फसलों के बीच सबसे कम है और शेष औसत 67 प्रतिशत नत्र पर्यावरण में खो जाता है। एरोबिक स्थितियों में ज्यादातर नत्रजन उर्वरक क्रियाकलाप

नाइट्रेट के रूप में धारण करती है, परंतु अक्षम लक्षणप्रारूपी चयन और कम प्रभावी नत्रजन सहनशीलता की जाँच की कठिनाई कार्यप्रणाली में नत्रजन उत्तरदायी किस्मों के विकास को जटिल करती है। इसलिए, एरोबिक खेती के तहत अधिक उपज और नत्रजन उपयोग दक्षता (नाइट्रेट के रूप में) के हेतु उपयुक्त धान की किस्मों की पहचान करने के साथ-साथ आनुवंशिक विश्लेषण करने के उद्देश्य से वर्तमान अध्ययन किया गया है।

लक्षणप्रारूपी चयन के लिए इस परिक्षण में 123 प्रकार के धान के लाइनों को सम्मानित किया गया, जिस में, अनुमोदित किस्मे, उन्नत प्रजनन लाइनों, देशी किस्मों और तुलनात्मक किस्मों को तीन विभिन्न उपचारों जैसे की, शुन्य नत्रजन (N^0), नत्रजन कैल्शियम नाइट्रेट (NO_3^-) के रूप में और नत्रजन अमोनियम क्लोराइड (NH_4^+) के रूप में ऑगमेंटेड डिजाइन में एरोबिक और एनारोबिक स्थितियों में खरीफ 2015 के दौरान आनुवंशिकी एवं पादप प्रजनन विभाग, संशोधन सह निर्देशात्मक फार्म, इं. गा. कृ. वि., रायपुर में लगाया था। इस परिक्षण के लिए निर्धारित खाद की मात्रा 80:60:40 नत्रजन, स्फुरद, पोटैश किलो प्रति हैक्टर का उपयोग किया गया है। उपज एवं अन्य महत्वपूर्ण लक्षणों के आधार पर 38 लाइनों का चुनाव किया गया और खरीफ 2016 के दौरान एरोबिक और एनारोबिक दोनों स्थितियों के तहत तीन उपचारों और दो यदन्धिक (replication) के साथ श्री वे फैक्टोरियल डिजाइन का उपयोग किया गया। इस परिक्षण से आनुवंशिक घटकों का जैसे की लक्षणप्रारूपी गुणांक विभिन्नता (PCV), जीनप्रारूपी गुणांक विभिन्नता (GCV), आनुवंशिकता, आनुवंशिक अधिकता, सहसंघ गुणांक एवं पथ गुणांक और स्थिरता विश्लेषण का अध्ययन किया गया है।

श्री वे फैक्टोरियल विश्लेषण के अध्ययन से पता चला की सभी लक्षणों के लिए लाइनों के बीच सकारात्मक आनुवंशिक विविधता की उपस्थिति हैं जो की धान उपज और नत्रजन उपयोग दक्षता उन्नयन कार्यक्रमों में किया जा सकता है। अध्ययन के तहत उपज और नत्रजन ($G \times N$) इंटरैक्शन घटकों के लिए किस्मों में महत्वपूर्ण परिणाम पाया गया था। NH_4^+ और NO_3^- के डायनामिक्स के प्रवृत्ति विश्लेषण से ज्ञात हुआ है कि एनारोबिक स्थिति में NH_4^+ सांद्रण अधिक प्रभावी रहा, जब कि एरोबिक परिस्थिति में NO_3^- प्रभावित रहा। किस्मों की औसत प्रदर्शन से ये पाया गया है की, उपज और नत्रजन की मात्रा विभिन्न स्थितियों में NO_3^- और N^0 की तुलना में NH_4^+ में अच्छा परिणाम दिखा गया है।

एरोबिक स्थिति में सर्वोच्च अनाज उपज और नत्रजन उपयोग दक्षता की मात्रा किस्म आर.पी. 5125-2-4 द्वारा 244.35, 278.82 और 310.76 ग्राम/मी² क्रमशः N^0 , NO_3^- और NH_4^+ में पायी गई है। इसी तरह आई.आर.-64 (सूखा) (227.11, 268.17 और 300.62 ग्राम/मी²) और आर.ए.यू. 1484-एयर-04 (200.75, 241.31 और 262.60 ग्राम/मी²) में भी क्रमशः N^0 , NO_3^- और NH_4^+ में सर्वोच्च अनाज उपज और नत्रजन उपयोग दक्षता की मात्रा पायी गई है। इस किस्म ने

एरोबिक और एनारोबिक स्थिति दोनों के लिए अलग-अलग नत्रजन के तहत स्थिर प्रदर्शन दिया था। आर.सी.पी.आर. 8, सी.आर. 3634-1-3 और आर.पी. 5125-2-4 एरोबिक स्थिति के लिए N^0 , NO_3^- और NH_4^+ तहत सबसे ज्यादा दाना में नत्रजन और प्रोटीन की मात्रा मिली है। लक्षणप्रारूपी गुणांक विभिन्नता (PCV) सभी अध्यनरत लक्षणों के लिए जीनप्रारूपी गुणांक विभिन्नता (GCV) की तुलना से अधिक है। जो की यह दर्शाता है कि विभिन्नता जीनप्रारूप के कारण नहीं है बल्कि पर्यावरण के प्रभाव के कारण भी है।

विभिन्न नत्रजनो तथा विभिन्न स्थितिओ में पौधों की ऊंचाई, जैविक उपज, फसल सूचकांक, अनाज नत्रजन उपज, पुआल नत्रजन उपज, बायोमास नत्रजन उपज, नत्रजन फसल सूचकांक, नत्रजन तेज दक्षता और नत्रजन उपयोगिता दक्षता के लिए उच्च आनुवंशिकता के साथ उच्च आनुवंशिक अधिकता पायी गई है। इससे संकेत मिलता है कि इन लक्षणों को मुख्य रूप से संयोजी जीनक्रियाओं द्वारा नियंत्रित होती है और चयन के लिए अधिक उपयोगी है। इन लक्षणों ने सकारात्मक सहसंबंध गुणांक और साथ ही अनाज की उपज पर प्रत्यक्ष प्रभाव दिखाया गया था, इससे पता चलता है कि उनके बीच वास्तविक सहसंबंध गुणांक है और इन लक्षणों को उपज सुधार के लिए प्रत्यक्ष चयन के लिए ले सकते हैं। किस्म सी.आर. धान 40 में एरोबिक और एनारोबिक वातावरण दोनों के लिए अलग-अलग नत्रजन व्यवस्थाओं के तहत स्थिर जिनक की मात्रा (भूरे और पॉलिश धान के अनाज में) पायी गई हैं।

दूसरे परिक्षण में 32 रेकॉम्बिनेंट इनब्रीड लाइन्स (स्वर्णा X बासमती-370 के बीच) में उपज के आधार पर चयन किया गया। इन जनक के साथ 32 लाइन्स का मार्कर विश्लेषण के लिए उपयोग किया गया हैं। परिणाम से पता चला है कि पौध की ऊंचाई के लिए 5 QTLs पहचाने गए हैं, जिनमें से गुणसूत्र # 5 पर 3 जीन है और गुणसूत्र # 8 और # 9 पर 1-1 जीन हैं। धान की पत्तियों में क्लोरोफिल सामग्री के लिए 4 QTLs की पहचान की गई है। अनाज उपज के लिए गुणसूत्र # 1 और # 5 पर 2 QTLs पहचान किए गए हैं। उपज के लिए एरोबिक स्थिति के लिए सभी नत्रजन व्यवस्थाओं के तहत गुणसूत्र # 5 पर मार्कर RM-18616 काफी महत्वपूर्ण पाया गया था।

यह अध्ययन एरोबिक और एनारोबिक स्थितियों के तहत NO_3^- और NH_4^+ में बेहतर नत्रजन उपयोग दक्षता किस्मों के पहचान और उत्पादन करने में सहायता करता है, जो खेती के लिए इस्तेमाल किया जा सकता है और भविष्य में पादप प्रजनन कार्यक्रम में जनक के रूप में इस्तेमाल किया जा सकता है।

CHAPTER - I

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's largest cultivated food crop. Rice is a member of family Poaceae and finds its home in South-East Asia and Asia, where more than 90% of world's rice is produced and consumed (Li and Xu, 2007). Rice is a main staple food diet of about 2.7 billion people and it needs to be produced 50% more than what is produced now by 2050 to overcome with the growing demand (Ashikari *et al.*, 2005). A major part of rice production is produced and consumed in Asia (Fageria, 2001). China and India are major rice-producing and consuming countries. The global production of rice has been estimated to be at the level of 740.9 million tonnes and the area under rice cultivation is estimated at 165.1 million hectares (FAOSTAT, 2016). India has 43.86 million hectares area under cultivation and production up to 104.80 million tonnes during 2014-15. Chhattisgarh (C.G.) the south east central state is also called the "Rice bowl of India". Total area of rice in C.G. is 3.80 million ha, production is 6.32 million tones and productivity is 1660 kg/ha in 2014-15 (Anonymous, 2015).

Classification of rice ecosystems is based on environmental conditions. The main environmental conditions considered in classifying rice ecosystems are soil moisture regime, soil drainage, land topography and temperature (IRRI, 1984). In India, rice farming is practiced in several agro-ecological zones and has cultivated in four distinct types of ecosystems: irrigated, rainfed upland, rainfed lowland and flood prone.

Rice is a wetland crop adapted and evolved under anaerobic conditions. Faced with scarcity of water resources, soil moisture stress is the single most critical threat to rice production thus affecting world food security (Farooq *et al.*, 2009). Moisture stress or soil water deficit that reduces nutrient availability to the plant (Oliver *et al.*, 2011). Plant species and genotypes of a species may vary in their response to mineral uptake under water stress. Haefele *et al.* (2008) strengthen the conception of water and nutrient stress as two major constraints in most rice-based rainfed system in Asia.

However, bottlenecks of water scarcity have been chased and breeders even developed a new plant type “aerobic rice” targeted at water limited rice environment (Atlin *et al.*, 2006). Upland rice also known as aerobic rice is mainly grown in Latin America, Africa and Asia. Area under aerobic rice cultivation has been increased and in future it is likely to cover major area as a new way of cultivating rice that requires less water than lowland rice.

Among essential plant nutrients, nitrogen (N) is one of the most yield limiting nutrients for upland rice production. Nitrogen fertilizer applied in the form of urea as it is the main nitrogen carrier worldwide in annual crop production. Predominant form of nitrogen (N) changes with change in water availability. Plant-useable N is consumed as nitrate (NO_3^-) from aerobic soils and as ammonium (NH_4^+) from flooded wetland, anaerobic soils (Huang *et al.*, 2000). When the field is drained and the soil becomes aerobic, ammonium is oxidized through microbial processes (known as nitrification) into nitrate (NO_3^-). Nitrification, is a dominant process in the N cycle and often determines the agronomic N use efficiency (NUE) of crops grown under unsaturated soil conditions, such as in aerobic cultivation (Barnard *et al.*, 2005 and Gujer, 2010).

The doubling of rice food production over the past decades has been associated with increase in the vast use of nitrogen fertilizers. To achieve better yield, farmers use to put elevated dosage of nitrogen fertilizers which generally support crop growth dynamics. As consequences, regular use of heavy chemical fertilizers based on nitrogen supply may impair soil health, which may not sustain crop production even after using heavy dosage of the nitrogen fertilizers. The excessive use of nitrogen fertilizers resulted in decrease of physiological nitrogen use efficiency (NUE) and cause serious environmental pollution (Jiang *et al.*, 2005). The current average nitrogen use efficiency (NUE) in the rice field is approximately 33%, poorest among cereals and a substantial proportion of the remaining 67% is lost into the environment (Hakeem *et al.*, 2012).

Grain yield in rice plant commonly affected by less nitrogen (N) nutrient in the soil due to its characters that easy to leaching, Less N conditions is common in all regions due to volatilization (Zhong-cheng *et al.*, 2012), denitrification, erosion, run-

off and absorbed by plants (Choudhury and Kennedy, 2005) or recovered in crop about 22%–30% of the applied N (Mei-hua *et al.*, 2012). It is unconscious that tolerant rice variety in poor-nitrogen soil or have nitrogen use efficiency is necessary. NUE at the plant level includes nitrogen uptake and assimilatory processes, redistribution within the cell and balance between storage and current use at the cellular and whole plant level. Rice genotypes show significant variability for N uptake (external efficiency) and N utilization (internal efficiency) with yield being predominantly determined by the uptake process, particularly under low-N conditions (Witcombe *et al.*, 2008).

Due to the roles of root in water and mineral uptake, it is one of the most important organs for rice growth in aerobic condition and it form one of the important components in nitrogen limiting soil. Genotype with a deep root system is beneficial in absorbing nutrient from soil. The correlation between morphological attributes and nitrogen uptake rates has been proven (Zaharath and Hanafi, 2009). A thick and deep root system has a positive bearing on rice performance (Yadav *et al.*, 1997). Therefore, the development of large root systems in rice has been, generally, suggested as one of the necessary factors to increase the rice grain performance.

The advent of molecular markers assisted technology and molecular linkage genetic maps have made it possible to characterize the performance of individual QTLs. These techniques have been widely applied to identify QTLs controlling yield and its related traits. The most important rice traits such as grain yield and quality have been focused to utilize QTL analysis (Yu *et al.*, 1997 and Yoon, *et al.*, 2006). Diverse rice genetic backgrounds in different environment allow the identification of a number of QTLs providing breeders information to improve breeding strategies via marker-assisted selection (MAS). For quantitative traits such as yield, a single QTL rarely accounts for a significantly large portion of the trait variation. Several QTLs with additive effects need to be stacked to achieve significant improvement. Recently, a large effect of *qtl12.1* and *qtl 1.1* etc. has identified to increased yield.

For the past years, attention has increasingly been paid to rice breeding with high N efficiency all over the world with the awareness of environmental protection.

The breeding and extension of rice with high N efficiency are attempted to decrease N application and alleviate the ecological problems with N fertilizer (Ladha *et al.*, 1998 and Jiang *et al.*, 2003). Therefore, the measurement and assessment of N losses and increased N use efficiency have been of great significance for sustainable agriculture and environmental protection. Moll *et al.* (1982) recommended selecting cultivars with high NUPE and NUTE. Samonte *et al.* (2006) also indicated that NUE should be considered during developing rice cultivars and making fertilizer N recommendations as well. In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. But rice is the only cereal crop cooked and consumed mainly as whole grains and consumers are mainly concerned with post-cooking quality of rice. Hence, quality considerations are more important (Hossain *et al.*, 2009).

The fulfill objective requires for comprehensive knowledge and deep understanding of the morphological and physiological of rice genotypes under different nitrogen regimes. In the present investigation, an attempt has been made to identify efficient rice genotypes in response to grain yield and nitrogen use efficiency (in the form of nitrate) under aerobic cultivation and morphological characterization of their root system. Keeping in view all the above facts the present study was planned with the following objectives.

The objectives of the present study are:

1. Screening and identification of rice genotypes for response to different forms of nitrogen under aerobic condition.
2. To study the grain quality characteristics and zinc content of selected rice genotypes.
3. Phenotyping of selected rice genotypes for root traits in mini-rhizotron.
4. Stability analysis for grain yield under differential nitrogen regimes.
5. Genotyping of rice genotypes with SSR markers.
6. Identification of QTLs in mapping population for grain yield in response to ammonium and nitrate.

CHAPTER - II

REVIEW OF LITERATURE

In this chapter, an attempt has been made to review the available literatures on genetic mechanism of yield, NUE and their contributing traits in rice. The available literatures have been classified into following headings:

- 2.1 Water deficit and their impact on grain yield and nitrogen use efficiency
- 2.2 Genetic variability of grain yield and improving NUE
- 2.3 Association studies in relation to grain yield and nitrogen use efficiency
- 2.4 Heritability
- 2.5 Root characteristics
- 2.6 Assessment of stability for grain yield
- 2.7 Quality parameters
- 2.8 Molecular markers and diversity analysis
- 2.9 Identification of quantitative trait loci for grain yield and its components

2.1 Water deficit and their impact on grain yield and nitrogen use efficiency

The first process affected by water deficit is the development of foliar and expansion (Fischer and Hagan, 1965). As leaves are the vegetative organs that display higher N content during early developmental stages, N demand is also drastically reduced in early water deficits. Furthermore, during exponential growth, when the soil is not fully covered, drought restricts the active photosynthetic surface area, which causes a reduction in carbon assimilation and transpiration (Durand *et al.*, 1991).

Puckridge and O'Toole (1980) showed that biomass production of rice is a function of water use. The shortage of water in the soil suppresses the leaf expansion, tillering and photosynthetic rate along with leaf area due to senescence. All these factors are responsible for reduction in dry matter accumulation.

Row and Venkateswarlu (1983) studied the yield component of rice varieties viz., Rasi and IR-20 under moisture condition. The reproductive and ripening phase were vulnerable and crucial for moisture stress, which resulted in permanent damage to growth and yield.

Root mass changes under water deficit may be overestimated because of the restriction of root fragmentation and destruction by soil organisms, which depend on soil water content. However, some authors have found that the root growth of rice increased under water deficit (Ingram *et al.*, 1994). An increase in root depth penetration has also been reported in rice (Mambani and Lal, 1983). By contrast, Yamauchi *et al.* (1996) observed a reduction in root growth as a result of drought. Engels *et al.* (1994) found that drought reduced root growth near the soil surface but enhanced it at lower levels. Onillon *et al.* (1995) stated that the effect of water deficit on root dry weight was dependent on N fertilizer application.

Wopereis *et al.* (1996) reported that water stress during flower induction and inflorescence development leads to delay in flowering (anthesis) or even to complete inhibition as apical morphogenesis is sensitive to water deficit. Jongdee *et al.* (1997) reported that late season drought contributed to yield loss between 13% and 35%.

Pantuwan *et al.* (2002) reported that the water stress developed prior to flowering generally delayed the flowering of genotypes. Sharma and Singh (1999) reported that total nitrogen uptake influenced grain yield by producing higher percentage of filled spikelets (around 90%) as a result of spikelet degeneration decreases linearly with increasing nitrogen content in leaf at anthesis.

Oji and Izawa (1970) found that $\text{NO}_3^- \text{N}$ was converted to proteins at the same rate as $\text{NH}_4^+ \text{N}$ in young rice seedlings, but $\text{NO}_3^- \text{N}$ was not absorbed or assimilated as effectively as $\text{NH}_4^+ \text{N}$. Nitrogen transformation processes closely depend on water and its mobility in soil (Keller, 2005). The size of soil NO_3^- and NH_4^+ pools reflects the balance between various fluxes which results from several soil processes viz; plant N uptake, mineralization, immobilization, nitrification and losses to the atmosphere following denitrification and volatilization (Lemaire *et al.*, 2004). Mineralization, immobilization and nitrification are affected by content of water in soil (Gorissen *et*

al., 2004 and Lemaire *et al.*, 2004). Austin *et al.* (2004) demonstrated that mineralization was activated by a water pulse after a drought period.

During its life cycle, a plant may be subjected to a water deficit, an N deficit or a combination of both, thus co limiting (Sadras, 2005) its productivity. Under water scarcity, N demand by plants is reduced, as growth rate is diminished. If the effects on N supply is greater than that on plant growth, the result will be an N deficiency. The implications of this demand/supply duality can be observed when different species exhibiting contrasted growth rates are compared under similar conditions (Gonzalez-Dugo *et al.*, 2005). This series of direct and indirect (via N limitation) affects of water shortage on plant growth makes any quantification of the effect of water deficit on N nutrition a complex task.

Deshmukh *et al.* (2007) observed that in rice, water stress during flowering reduced the harvest index by as much as 60 %, largely as a result of a reduction in seed set. Nitrogen management practices played important roles in continuous aerobic rice cropping system. It was reported that N application significantly alleviated continuous cropping obstacle of aerobic rice (Nie *et al.*, 2008).

Li *et al.* (2009) found that N-use efficiency was increased by water deficit and diminished by the dose of N applied. Primoradian *et al.* (2004) reached the same conclusion in rice but the effect was only significant at particular level of N. Gonzalez-Dugo *et al.* (2005) showed the variability in resulting N status in two forage species displaying contrasting growth rates and root architecture when water and N are both limited. The effect of water deficit on plant N recovery capacity and on N-use efficiency was reviewed by Aulakh and Malhi (2005).

As a function of multiple interacting genetic and environmental factors, NUE is inherently complex. N use, grain yield and N accumulation, N in aboveground plant biomass, N harvest index, and grain N accumulation are the key indicators of N use efficiency (Huggins and Pan, 2003). The definition of NUE itself is also complex, and the term can mean different things in different contexts, including N use efficiency (NUE), N uptake efficiency (NUpE), N utilization (assimilation) efficiency (NUE), apparent N recovery rate (ANR), agronomy efficiency of fertilizer N (AE), N

physiological use efficiency (NpUE), N transport efficiency (NTE), and N remobilization efficiency (NRE). In general, two plant physiological components—NUpE and NUtE—contribute to plant NUE (Xu *et al.*, 2012).

2.2 Genetic variability of grain yield and improving NUE

Sattelmacher *et al.* (1994) pointed out that genotypes might differ in nitrogen use efficiency and uptake efficiency: the two factors that are attributed to genetic variation in nutrient efficiency in crops. Rice breeders have historically not included nitrogen utilization efficiency (NUtE) as a selection criterion in breeding for cultivars. Genotypic differences in response to nitrogen fertilizers and nitrogen utilization have been previously reported by (Broadbent *et al.*, 1987; Cho and Koh, 2005; De Datta and Broadbent, 1990; Park and Mok, 1975; Seo *et al.*, 2005).

Inthapanya *et al.* (2000) studied the genotype differences in nutrient uptake and utilization for grain yield production of rainfed lowland rice and reported the presence of significant genotypic variation in nutrient-use efficiency.

Fageria and Barbosa (2001) reported that shoot dry weight, grain yield, number of panicles, number of grains per panicle, 1000 grain weight, spikelet sterility, N uptake in grain, N harvest index and N use efficiency were significantly affected by genotype and N treatments. Genotypes x N interactions were only significant for shoot dry weight and spikelet sterility. Non-significant interactions between genotype and N level for most of the yield and yield components and N uptake parameters suggested that lowland rice genotypes can be evaluated for N use efficiency at a single N level. Correlation analysis showed that shoot dry weight, number of panicles, number of grains per panicle, grain harvest index, N uptake in shoot and grain, N harvest index, and N use efficiency having significant positive association with grain yield.

Swain *et al.* (2006) assessed variability in N uptake and utilization of medium and late duration rice varieties. They observed that difference in optimum yield of the medium and late duration varieties was due to the differences in the amount of N uptake and its use efficiency by the plant for grain production.

Manzoor *et al.* (2006) studied the effect of different N levels on yield and yield

components of basmati. According to results plant height, no. of productive tillers, panicle length, no. of grains per panicle, thousand grain weight and yield showed different trend with different N level. Similarly, Chaturvedi (2005) conducted field trial to determine the effect of different nitrogenous (N) fertilizers on growth, yield and quality of hybrid rice of different rice cultivars.

Gholizadeh *et al.* (2009) established relationship between N content and SPAD values using geostatistical tools. Analysis of variance, variogram and kriging were conducted to determine the variability of the measured parameters and also their relationship. Chlorophyll content in a leaf is closely correlated with leaf N concentration (Felix *et al.*, 2002).

Hassan *et al.* (2009) reported the genotypic variation in traditional rice varieties for chlorophyll content, SPAD value and nitrogen use efficiency. Nitrogen % in both straw and grain, nitrogen uptake by straw and grain, total nitrogen uptake and NpUE showed significant differences due to variable nutrient levels at maturity in traditional rice varieties. Significantly higher NpUE without addition of nitrogen (Zero N) indicated the ability of utilization of the native nitrogen by traditional varieties. The higher NpUE in zero nitrogen treatment confirmed the ability of producing similar yield level as compared to added nitrogen treatment.

Namai *et al.* (2009) investigated varietal differences in dry matter production and NUpE using a wide range of rice varieties at an early growth stage. Overall, this study found that there are wide variations in NUpE among varieties with similar levels of relative dry weight (RDW) under varying nitrogen conditions. Variations in NpUE were greater under lower nitrogen conditions; in contrast, variations in RDW were greater under higher nitrogen conditions. These data, along with those of other studies, indicated differences in nitrogen use efficiency between Indica- and Japonica types, upland and lowland varieties, and landraces and improved types.

Zhang *et al.* (2009) studied grain yield and physiological N use efficiency in relation to the accumulation and redistribution of biomass and N in rice. Results depicted differences in biomass, N accumulation and N redistribution at the post-heading of rice cultivars.

Islam *et al.* (2009) showed that root, stem and hill⁻¹, TDM (total dry matter) hill⁻¹ and chlorophyll content in leaves, varies with varying rates of N applications.

Konnerup and Brix (2010) demonstrated the effects of inorganic nitrogen (N) source (NH_4^+ , NO_3^- or both) on growth, biomass, photosynthesis and N uptake rate of *Canna indica*. NH_4^+ fed plants had higher concentrations of N in the tissues and higher contents of chlorophylls in the leaves compared to NO_3^- fed plants suggesting a slight advantage of NH_4^+ nutrition.

Barracough *et al.* (2010) studied genotypic and environmental variation for nitrogen efficiency in wheat. Data revealed that presence of significant varietal differences in yield at all N-rates. Grain yield ranged from 2.1 to 11.8 t/ha (85% DM), grain %N from 1.1% to 2.8% (in DM), total-Nup from 31 to 264 kg-N/ha, grain-NutE from 27 to 77 kg-DM/kg-N and nitrogen harvest index was ranged from 69% to 98%. Yield was positively correlated with total N-uptake and N-utilization at each N rate.

Masclaux-Daubresse and Chardon (2011) reported that Single-seed dry weight and N concentration are robust traits, highly heritable, whereas GHI (grain harvest index) and NHI (nitrogen harvest index) are highly correlated and affected largely by N supply level and availability, particularly at the seed-filling stage. Higher NUE has been observed in cultivars with higher GHI (Bufogele *et al.*, 1997).

Singh and Verma (2013) characterized and screened high N efficient genotypes. The genotypes were screened on the basis of growth dynamics, physiological and agronomic responses to nitrogen rates. Results showed, traits associated with growth, physiological area index, photosynthetic rate, SPAD value, leaf N content and NR activity and agronomical traits enhanced significantly with increased N rates. Experiment concluded that among all genotypes, few are more proficient to assimilate N in their tissues. Therefore, more N efficient genotypes can be suggested to farmers for yield enhancement and reducing environmental pollution.

Abe *et al.* (2013) evaluated genetic variation for NUE among tropical maize hybrids selected for contrasting responses to N. Their results documented significant genetic variation for grain yield (GY) and measured NUE components among the

hybrids, as well as significant interactions between hybrid and N level for all traits except nitrogen harvest index.

Makhziah *et al.* (2013) ten genotypes of maize were studied in order to enhance the understanding of genetic basis of NUE. The results showed that genotypes exhibiting contrasted responses to N nutrition. Nitrogen deprivation caused varied reductions of plant height, leaves area, chlorophyll content, stay green, N uptake, total dry matter, grain yield, grain number and a thousand grain weight among genotypes; but did increase days to 50% anthesis, 50% silking, anthesis-silking interval, crop recovery efficiency of applied N (REN), physiological efficiency of applied N (PEN), agronomic efficiency (AE) and NUE significantly ($P = .05$).

Tadesse *et al.* (2013) an experiment was carried to assess the effect of nitrogen labels and genotype by nitrogen interaction. Results showed highly significant variation ($P < 0.0001$) among the genotypes for NUE and yield traits studied. The presence of such variation indicates that efficient and high yielding malting barley genotypes can be directly selected. Highly significant variation was observed between N-levels for most of the NUE traits in which higher value was obtained from the lower level of N. There was no significant interaction between N-levels and genotypes. High phenotypic coefficient of variation (PCV) was observed for UPE (34.57%) and NUE (31.6%). High genotypic coefficient of variation (GCV) was not observed for the studied traits. Of the traits of malting barley studied in this experiment, 50% show low heritability which makes selecting for these traits difficult because environmental effect is more evident than genetic effect. Therefore future breeding efforts in malting barley should aim at exploiting the genetic variability available in the test genotypes.

Kang *et al.* (2013) a field study was conducted to understand nitrogen use efficiency of high yielding Japonica rice varieties under three levels of nitrogen fertilizer (90, 150 and 210 kg N ha⁻¹) in Iksan, Korea. Result revealed that total N uptake (kg ha⁻¹) showed significant variations by nitrogen levels and varieties. Higher nitrogen levels accounted higher amount of nitrogen in grain which were ranged from 72.2 to 86.0 kg ha⁻¹. Nitrogen uptake efficiency (NUpE) and nitrogen use efficiency (NUE) showed significant differences while harvest index (HI), nitrogen harvest index

(NHI), and utilization efficiency (NUE) didn't varied significantly by nitrogen fertilizer level. Rough rice yield and panicle number per m² were significantly affected by nitrogen level, variety, and nitrogen level $\times$ variety interaction. 1000-grain weight was affected by variety, and nitrogen level $\times$ variety interaction. While number of spikelets was significantly affected only by variety.

Fageria (2014) reported significant variations of N use efficiency among lowland rice genotypes and suggest that nitrogen harvest index is an important index in determining crop yields because it is positively associated with grain yield. Furthermore, shown that N uptake in lowland rice grain and shoot had a significant positive relationship with grain yield. Isfan (1993) reported highly significant variation among oat genotypes in both yield and physiological efficiency of absorbed N.

Rao *et al.* (2014) demonstrated effect of different doses of nitrogen on performance of promising varieties of rice in high altitude areas of Andhra Pradesh. Tiller production, days to 50 per cent flowering, dry matter production at harvest, yield attributes, yields and harvest index, protein content of grain and available nitrogen were progressively augmented by incremental levels of N.

Kumar *et al.* (2014) revealed considerable variability among the RILs for all the traits under study. The phenotypic coefficient of variation (PCV) values was slightly greater than genotypic coefficient of variation (GCV), revealing negligible influence of environment in character expression except for number of unfilled spikelets per panicle. High heritability coupled with high genetic advance and high GCV were observed for number of leaves per plant, number of tillers per plant, number of productive tillers per plant, flag leaf width, panicles weight per plant, average panicle weight, number of spikelets per panicle, number of filled spikelets per panicle, spikelet fertility per cent, spikelet density, grain yield per plant, biological yield per plant and harvest index.

Kumar *et al.* (2014) carried physiological evaluation of NUE and yield attributes in rice genotypes under different N levels. Traits under study were plant height, no. of effective tillers, leaf area index, vegetative plant growth and grain yield. Owing to the performance of genotypes they suggested that these traits can be utilized

as physiological markers for the selection of rice genotypes efficient in N-use. Huang *et al.* (2016) suggest that Guiliangyou 2 is a unique super-hybrid rice cultivar that achieves high grain yield by increasing harvest index and N-use efficiency.

Malik *et al.* (2014) examined effect of different levels of nitrogen on growth and yield attributes of different varieties of Basmati rice. The parameters measured included plant height, number of tillers/hill, dry weight, length of panicle, number of filled grains / panicle, straw yield, biological yield, harvest index and grain yield. The varieties were evaluated under three nitrogen levels. The varietal trial indicated that Pusa Basmati- 1 at one nitrogen level was significantly different for all the parameters undertaken. Similarly, in recent study, Koffi *et al.* (2016a) evaluated yield and nitrogen use efficiency of aromatic rice varieties in response to nitrogen fertilizer.

Singh *et al.* (2014) field experiment was conducted to study the impacts of increased nitrogen doses on growth dynamics, biomass partitioning, chaffy grain and nitrogen use efficiency in rice genotypes. Result revealed that chaffy grain number and chaffy grain weight per 5 panicles was significantly increased with enhancing nitrogen doses. In addition to this, a significant correlation between nitrogen doses and growth dynamics, biomass partitioning and chaffy grain was observed. These findings suggest that growth dynamics, biomass partitioning, chaffy grain could be enhanced by the input of high rate of nitrogen fertilizer but not nitrogen use efficiency. Therefore, this study is useful to screen most N efficient genotypes which can be strongly suggested to rice growers to enhance crop yield irrespective of use of high dose of N fertilizers

Haque and Haque (2016) evaluated growth, yield and nitrogen use efficiency of new rice variety under variable nitrogen rates. From the results it was concluded that growth, yield and nitrogen use efficiency of the new rice variety were significantly influenced by different levels of nitrogen fertilizer. Although growth of the variety increased with increased nitrogen levels, assimilate mobilization towards grain was higher at 60 kg N ha⁻¹. Consecutively, the variety produced the highest yield with 60 kg N ha⁻¹ with the highest nitrogen use efficiency.

Koffi *et al.* (2016b) field experiments were conducted at Ndiaye and Fanaye (Senegal) during the hot and dry season 2012 and the wet season 2012 to evaluate the effect of nitrogen on rice yield and nitrogen use efficiency under phosphorus and potassium omission management. Results showed that across genotypes, rice yield varied from 3.3 to 8.6 Mg/ha under N-P fertilizer and from 3.5 to 8.8 Mg/ha under N-P-K fertilizer at Ndiaye. At Fanaye, rice yield varied from 3.7 to 8.6 Mg/ha under N-P fertilizer and from 3 to 10.3 Mg/ha under N-P-K fertilizer. The PFPN and the ANUE were influenced by genotype and varied from 161 to 28 kg grain/kg N and from 105.9 to 0.9 kg grain/kg N, respectively. The highest PFPN was obtained by Sahel 108 followed by Sahel 177. K addition to N-P significantly increased ANUE from 6.4 to 20.78 kg grain/kg N.

Zhu *et al.* (2016) reported that the total N uptake significantly increased ($p < 0.01$) along with the year of release, and the values ranged from 138 to 208 kg ha⁻¹ in 2013 and from 150 to 248 kg ha⁻¹ in 2014. The N harvest index (NHI) ranged from 33.9 to 62.2% in 2013 and from 48.8 to 65.0% in 2014. In 2013, the correlation between the NHI and the year of release was significant at $p < 0.01$ ($R^2 = 0.48$), whereas in 2014, the correlation was significant at $p < 0.1$ ($R^2 = 0.22$). Both the total N uptake and NUEg significantly contributed to the increased grain yield at $p < 0.01$ in 2013 and 2014.

Naveen Kumar and Uma (2016) field screening of 55 local rice genotypes were conducted under low and no nitrogen conditions revealed highly significant genotypic differences for all the traits studied. High genotypic coefficient of variability and phenotypic coefficient of variability values with less difference observed for nitrogen use efficiency, yield and quality related traits indicating less influence of environment factors on their expression. High heritability coupled with high genetic advance was recorded for plant height, number of productive tillers, panicle length, panicle weight, number of spikelets per panicle, test weight, grain and straw yield per plant, nitrogen use efficiency, grain quality traits and protein content at both low and no nitrogen conditions. This indicated that these traits were predominantly controlled by additive gene action and more amenable for selection.

Significant positive correlation of nitrogen use efficiency with grain and straw yield in both low and no nitrogen conditions was observed.

2.3 Association studies in relation to grain yield and nitrogen use efficiency

Garrity and O'Toole (1994) reported that grain yield, relative grain yield and spikelet fertility were significantly and negatively related to the number of days after the beginning of the stress period that a cultivar flowered. Percentage spikelet fertility was highly correlated with grain yield under reproductive stage water stress. Spikelet fertility was the most practical character by which to score cultivar performance.

Rice breeders have historically not included nitrogen utilization efficiency (NUE) as a selection criterion in breeding for cultivar. For achieving higher yield use of nitrogen efficient genotypes is an important complementary strategy in improving rice yield and reducing cost of production in subsistence farming. Results of several studies have indicated that application of N fertilizer increases grain yield of rice by increasing the magnitude of its yield attributes (Panda *et al.*, 1995).

Jongdee *et al.* (1997) found that only biological yield and harvest index were found to be significantly associated with grain yield under drought treatments.

Babu *et al.* (2003) reported positive correlation of biomass under stress with yield, per cent spikelet fertility, number of seeds per panicle, harvest index and relative yield. On the other hand, leaf rolling scores had negative correlation with yield and harvest index.

Kumar *et al.* (2004) observed that in rice there is a negative association between delay in flowering and grain yield, relative water content and post flowering dry matter production under rainfed condition.

Lafitte *et al.* (2004a) found negative correlation between plant height and yield. Tall lines yield poorly in rainfed experiment but no significant association was observed between yield and height under control condition.

Lanceras *et al.* (2004) used double haploid mapping population to measure correlation between traits and grain yield at different water levels and reported

correlation between grain yield and biological yield ranges 0.70 to 0.54, indicated that genetic improvement in the grain yield would likely be accompanied by improvement of biological yield.

Rajeshwari and Nadarajan (2004) observed positive correlation between numbers of filled grains per panicle and grain yield.

Singh *et al.* (2004) reported significant and positive correlation between grain yield per plant and yield contributing traits, effective flag leaf breadth and total seeds per panicle. A negative correlation was found between grain yield and plant height.

Verulkar *et al.* (2004) reported positive correlation of spikelet fertility, harvest index and biological yield with yield under stress.

Under well-watered conditions, Lanceras *et al.* (2004) observed a high genetic association for biological yield, harvest index, days to flowering after initiation of irrigation gradient, percent spikelet fertility, total spikelet number, plant height, and grain yield.

Gomez *et al.* (2006) reported positive and significant correlation of panicle length and number of productive tillers with grain yield under stress. They also observed positive correlation of root traits with plant height under stress. Similar relation was also reported earlier in rice by Venuprasad *et al.* (2002).

Samonte *et al.* (2006) examined the significance and magnitude of variation in N content, NUE, N translocation ratio (NTR), and grain protein concentration among diverse rice genotypes. Nitrogen content and NUE were not significantly correlated with each other, and they had significant positive direct effects on grain yield. Grain yield was positively correlated with NUE, N content, and NTR, whereas NTR was correlated with grain protein concentration. Plant breeders could use these significant correlations to their advantage in breeding for rice cultivars that not only produce high yield but also utilize N efficiently and produce grain with a higher protein concentration.

Prudente *et al.* (2008) reported higher correlations ($p=0.001$) between the yield ($r = 0.96$; $r = 0.99$), number of panicles ($r = 0.98$; $r = 0.96$) and number of tillers ($r =$

0.96; $r = 0.97$) and N uptake ($r = 0.97$; $r = 0.95$) of *japonica* and *indica* rice varieties and applied N, respectively.

Sun *et al.* (2009) and Sun *et al.* (2012) who investigated the relationship between yield and NUE. Correlation analysis revealed that the grain yield was significantly related to the N uptake and utilization, and that the root activity was significantly related to the ammonium assimilation enzymes and photosynthetic rate. These results suggest that the N application strategy should be adjusted according to different irrigation regimes in order to obtain the highest yield and the best NUE.

Tari *et al.* (2009) investigated nitrogen chlorophyll condition at different nitrogen fertilization methods in rice by applied mathematics relations with use of chlorophyll meter, at different growing stages of rice. Their results showed that the SPAD reading at all stages was positively correlated with rice yield that illustrated the importance of chlorophyll content and its related to grain yield.

Umadevi *et al.* (2009) reported that grain yield per plant was positively and significantly associated with days to 50 % flowering, number of productive tillers per plant, number of secondary branches per panicle and straw yield.

Fu *et al.* (2010) reported significant positive correlations of grain yield per plant with spikelets per panicle, 1000 seeds weight, and number of panicles per plant and percentage seed set. The number of seeds per panicle also had strong positive correlations with percentage seed set, but the number of panicles per plant had significant negative correlations with spikelets per panicle, seeds per panicle and 1000 seeds weight. In addition to this, there was a significant negative correlation between panicles per plant and percentage seed set.

Nandan *et al.* (2010) revealed strong positive association of yield with days to 50 % flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility. The result of path analysis indicated that the number of grains per panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking, days to 50 % flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking. He also reported Negative correlation of 1000 grain weight with grain yield.

Gomez *et al.* (2010) reported significant positive correlation between plant height and biomass under stress. Significant negative correlations were noticed for water stress indicators such as leaf rolling and leaf drying and positive correlations for plant production traits with biomass have been reported in rice. It was also reported by Babu *et al.* (2003) and Gomez *et al.* (2006).

Fu *et al.* (2010) reported significant positive correlations of grain yield per plant with spikelets per panicle, 1000 seeds weight, number of panicles per plant and percentage seed set; whereas number of panicles per plant had significant negative correlations with spikelets per panicle, seeds per panicle and 1000 seeds weight.

Frageria *et al.* (2011) reported that shoot dry weight and grain yield significantly ($P < 0.01$) increased in a quadratic fashion when N rate increased by ammonium sulphate as well as urea fertilization. Maximum grain yield at average N rate was 22% higher with the application of ammonium sulphate compared to urea, indicating superiority of ammonium sulphate compared to urea. Plant height, shoot dry weight, grain harvest index, 1000 grain weight and N uptake and use efficiency in shoot and grain had significant positive association with grain yield. However, spikelet sterility was negatively associated with grain yield.

Abarshahr *et al.* (2011) reported significant correlation among paddy yield with plant height, panicle number per plant, flag leaf width, number of filled grains per panicle, number of spikelet per panicle and 1000-grain weight ($p < 0.01$), panicle length, brown grain length a day to complete maturity and chlorophyll index ($p < 0.05$) under optimum . correlations under drought stress conditions showed that, paddy yield had significant and positive correlation with plant height, panicle length, number of panicles per plant, flag leaf width, days to 50% flowering, number of filled grains per panicle, number of spikelet per panicle, 1000-grain weight ($p < 0.01$), flag leaf length, brown grain width, panicle fertility percentage and chlorophyll index ($p < 0.05$) while correlation between paddy yield and plant height or paddy yield and days to 50% flowering were negative

Ekka *et al.* (2011) conducted association analysis studies and revealed that grain yield per plant had positive significant correlation with leaf width, days to 50%

flowering, plant height, panicle length, number of filled grains per panicle, 100 seed weight and paddy (grain) length.

Haider *et al.* (2012) reported that root length, root shoot ratio, thousand seeds weight, seeds per panicle, spikelet fertility and drought response index showed positive and significant association with yield per plant under drought stress at genotypic level; whereas, leaf drying had significantly negative correlation with yield.

Kang *et al.* (2013) conducted study on high yielding japonica rice under three nitrogen levels. Rough rice yield showed linear relationship with total nitrogen uptake within the range of nitrogen treatments. Rice varieties showed different nitrogen uptake ability and NUE at different nitrogen level. Significant variations and relationships among grain yield, NUpE, and NUE confers an advantage to breeder and agronomist. The little information on NUE variability and its relationships with yield and yield related traits in rice has led to investigation of genetic variability in N use efficiency among upland rice genotypes, identifying genotypes with best N use efficiency and also assessing nature of association among N use efficiency and yield and yield related traits.

Gopikannan and Ganesh (2013) reported significant positive association of grain yield per plant with number of productive tillers per plant, panicle length, spikelet fertility percentage, number of filled grains per panicle, proline content, total chlorophyll content and chlorophyll stability index.

Kumar *et al.* (2014) studied correlation and path analysis and revealed that the traits such as panicles weight per plant, number of spikelets per panicle, panicle index, number of leaves per plant, plant height, days to heading, average panicle weight, flag leaf width, grain length and hulling % exhibited significant positive correlation with grain yield per plant as well as positive direct effects on grain yield per plant.

Shellammal *et al.* (2014) found that Plot yield under stress was significantly and positively correlated with harvest index and 1000-grain weight, but negatively associated with leaf rolling score and days to 50% flowering.

Islam *et al.* (2014) the objective of the study was to establish a relationship between leaf SPAD readings and grain yield of wheat grown under different fertilizer

management options. The SPAD values were positively correlated with grain yield at different growth stages. The highest correlation ($r=0.99^*$) corresponded to 70 days after sowing (DAS). The higher correlation coefficient value indicated that the SPAD values of flag leaves up to 96 DAS are important for predicting grain yield in wheat.

Lakew (2015) observed that the grain yield showed significant and positive correlation with grain nitrogen yield, and nitrogen harvest index. Grain nitrogen concentration had significant and positive correlation with nitrogen uptake efficiency and nitrogen use efficiency. Grain yield, harvest index, grain nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency had high genotypic and phenotypic coefficient of variation and high broad sense heritability estimates.

Zhu *et al.* (2016) study suggested that genetic improvements in rice grain yield are associated with increased NUE. Significant improvement in grain yield was obtained from increase in the harvest index and biomass, and spikelet per panicle. It can be concluded that concomitant relationship exist between grain yield and NUE.

Moosavi *et al.* (2015) found that grain yield per plant showed significant correlation with panicle number, harvest index, dry weight and panicle length these traits can be used as indicators for indirect selection of grain yield.

Xu *et al.* (2016) quantified yield gap and NUE of irrigated rice. Results obtained using the Pearson' correlation analysis showed significantly negative coefficients for yield response (YR) to soil nutrient contents and soil organic matter. The large variations in YR were attributed to differences in climatic conditions and soil indigenous nutrient supplies. They concluded that in order to narrow the YG and increase NUE, effective soil, plant, nutrient management measures, advances in knowledge and technologies would be required to sustain higher crop production.

2.4 Heritability

Babu *et al.* (2003) reported high heritability (broad sense) of leaf rolling, grain yield, plant height, spikelet fertility, harvest index and days to heading while, low to

moderate for relative water content, plant height, grain yield, biomass, spikelet fertility, seeds per panicle and 1000 seeds weight under stress.

Singh *et al.* (2004) observed high heritability of traits like grain yield and yield contributing character, suggesting that the importance of these traits as criteria for improving overall yield under stress. Moderate heritability was also observed for panicle length while low heritability for leaf breadth and test weight.

Karim *et al.* (2007) reported high heritability with high genetic advance in percent of mean (GAPM) was observed for 1000-grain weight followed by spikelet sterility (%) and number of filled grains per panicle

Kumar *et al.* (2008) reported heritability in broad sense for grain yield, harvest index, 50 % flowering, leaf rolling and leaf drying was 0.48, 0.45, 0.47, 0.20 and 0.42, respectively for IR55419 × IR64 and 0.45, 0.38, 0.73, 0.26 and 0.30, respectively for IR55419 × Way Rarem, derived progenies.

Srinivasan *et al.* (2008) reported heritability in broad sense of leaf rolling, days to flowering, plant height, panicle length, 1000 seeds weight, grain yield, biomass yield and harvest index was 0.63, 0.64, 0.48, 0.54, 0.63, 0.46, 0.51 and 0.27, respectively in doubled haploid (DH) line population from the cross CT9993-5-10-1-M × IR62266-42-6-2.

Venuprasad *et al.* (2009) reported heritability in broad sense under lowland stress was 0.73 in 2006 and 0.55 in 2007 for grain yield.

Bernier *et al.* (2009) reported heritability 0.75, 0.49, 0.54, 0.94 and 0.44 for grain yield, biomass yield, harvest index, days to 50 % flowering and plant height, respectively.

Umadevi *et al.* (2009) estimated high heritability in broad sense of days to 50 % flowering, plant height (cm), panicle length (cm), number of secondary branches/panicle, leaf length (cm), leaf width (cm), seed length (mm), seed breadth (mm), seed L/ B ratio, straw yield (g), 100 seeds weight (g) and grain yield per plant (g).

High heritability with high genetic advance as percent of mean was reported by Nandan *et al.* (2010) for number of effective tillers per plant, panicle weight, number

of grains per panicle, number of spikelets per panicle, 1000 grain weight, kernel length before cooking, length breadth ratio, water uptake ratio and grain yield per plant.

Verulkar *et al.* (2010) reported broad sense heritability of 50 % flowering (0.92 for control, 0.78 for moderate and 0.83 for severe drought), plant height (0.96 for control, 0.81 for moderate and 0.83 for severe drought), grain yield (0.55 for control, 0.52 for moderate and 0.73 for severe drought) and harvest index (0.58 for control, 0.56 for moderate and 0.78 for severe drought).

Akhtar *et al.* (2011) found heritability to be highest for number of grains per panicle, days to maturity, plant height and paddy yield while lowest for number of tillers per plant. Paddy yield had strong genetic correlation with number of grains panicle-1, days to maturity and 1000-grain weight.

Seyoum *et al.* (2012) reported high heritability for plant height, followed by 50 % flowering, 1000 seeds weight, panicle length, and spikelets per panicle, which indicated high heritable proportion of variation under rainfed upland rice.

Kiani (2013) reported high heritability coupled with high genetic advance found for total seeds per panicle, filled seeds per panicle, tiller number and grain yield make these traits suitable for selection.

Shellammal *et al.* (2014) reported that the plot yield, 1000-grain weight, panicle exertion and canopy air temperature difference exhibited high heritability under the control conditions, whereas spikelet sterility and single plant yield exhibited high heritability under the moderate stress conditions. Traits such as days to 50% flowering, plant height and osmotic potential showed high heritability under the severe stress conditions.

Shrivastava *et al.* (2014) reported that the traits viz., harvest index, biological yield per plant, flag leaf width, 1000 seed weight, plant height, flag leaf length, panicle length, decorticated seed width, seed width and seed length had high heritability accompanied with high genetic advance.

Khatun *et al.* (2015) reported highest heritability for photosynthetic rate, transpiration rate, number of filled grains/panicle and yields/plant (g).

Makhziah *et al.* (2013) heritability estimates (h^2) were high ($h^2 > 0.5$) for most of measured traits at all N levels and ranged from -0.892 to 0.998. This indicated that it is possible to select genotypes are adapted to low N under both low and high N fertilization. High genotypic variation for grain yield was observed at all N levels, while for REN, PEN and AE were found at high-N and NUE at low-N. Reduction of N level from 180 to 90, 30 and 0 kg N.ha⁻¹ caused reduction of 7.8%, 14.4% and 49.4% grain yields respectively.

2.5 Root characteristics

Root system development is an important target for improving yield in cereal crops. Active root systems that can take up nutrients more efficiently are essential for enhancing grain yield. The root morphological traits associated with the adaptation to N-depleted soils, the qualitative and quantitative importance of the root system in taking up N under N-limiting conditions has been pointed out in several studies (Guingo *et al.*, 1998; Kamara *et al.*, 2003; Coque and Gallais, 2006).

Gomez *et al.* (2005) observed that root thickness and root weight were positively correlated with root length; root thickness was significantly and positively correlated with root weight and biological yield; and plant height was positively correlated with grain number per panicle. Leaf area per plant showed the highest positive direct effect on root weight followed by biological yield and root thickness.

One of the main difficulties in evaluating the influence of the size, the volume, and the root system on NUpE and traits related to yield or grain N content is to remove the entire intact root system from soil when plants are grown under agronomic conditions (Kondo *et al.*, 2003). To solve this problem, alternative techniques have been developed under controlled environmental conditions using either 'rhizotrons' (Devienne-Barret *et al.*, 2006; Laperche *et al.*, 2006). Consequently, there are only a limited number of reports describing the response of the root morphology of cereals to different levels of N fertilization (Kondo *et al.*, 2003).

Although there are many several studies related to variation in N uptake in rice, there seems to be little information on differences in root morphology that may

contribute to this variation. Root characteristics such as root length density and root weight density have been identified as important factors because N uptake is determined by root mass and N uptake per unit root volume (Shimono and Bunce, 2009).

Mohankumar *et al.* (2011) reported that below ground traits roots traits has a direct relevance in improving grain yield under aerobic condition. Root traits such as root volume and root dry biomass were positively and significantly correlated with grain yield. Leaf characters such as total leaf area (TLA) also correlated significantly with grain yield.

Hamaoka *et al.* (2013) recently evaluated genetic variations in dry matter production, nitrogen uptake, N and water use efficiencies (NUE and WUE), bleeding sap rate (BR), and root morphological traits at vegetative stage in 6 cultivars and 4 strains of 6 species (*O. sativa*, *O. glaberrima*, *O. barthii*, *O. nivara*, *O. meridionalis*, and *O. rufipogon*) grown under different nitrogen conditions. Their results suggested that a high NUE is associated with the development of a root system, increased BR, and probably increased capacity of NO_3^- -N uptake.

Seyed Mostafa (2013) root study conducted in greenhouse, by using image analysis methods implemented in WinRHIZOPro system to analysis of the relationship between root morphology and uptake of fertilizer nitrogen in rice. The results showed significant differences in root length, surface area, volume and the number of forks among the studied cultivars. The amount of Nitrogen in plant organs (derived from fertilizer applied), was found to range from 24.05 in Tarom-e-Mahali to 56.67 % in Neamat cultivars. A significant correlation was observed among the surface area, total root length, No of forks, biological yield and the amount of fertilizer Nitrogen uptake. The Neamat and Tabesh cultivars performed efficiently in fertilizer Nitrogen uptake.

Thiem and Akira (2015) studied effects of nitrogen (N) application on root system development under different drought stress conditions. The experiments were conducted in a line source sprinkler system creating a soil moisture gradient under a rain-out shelter. Three N fertilizer treatments were applied: 60, 120 and 180 kg N ha⁻¹.

The obtained results showed that increase of N level from 60 to 120 kg N ha⁻¹ increased total root length and shoot dry weight of Nipponbare under severe drought stress conditions (<17% w/w of soil moisture content (SMC)) but did not increased those traits as increased N application from 120 to 180 kg N ha⁻¹. However, under mild drought stress (17- 25% w/w of SMC) and well-watered (>25% w/w of SMC) conditions, total root length increased with increased N application leading to increase stomatal conductance and photosynthetic rate, and eventually increased shoot dry weight. In addition, only under well-watered conditions the relationship between the total root length and shoot dry weight was positive and notably significant at 120 and 180 kg N ha⁻¹ levels but not at 60 kg N ha⁻¹ level. The experiment suggested that the nitrogen application levels of 120 and 180 kg N ha⁻¹ increased the dry matter production due to the increased total root length under well-watered conditions.

2.6 Assessment of stability for grain yield

Sawant *et al.* (2005) conducted stability assessment in late duration rice hybrids and reported that the mean sum of square due to environment (linear) was significant when tested against pooled deviation with respect to grain yield, indicated differences between locations and their influence on genotypes for expressing of character. This is in accordance with previous reports on rice by Panwar *et al.* (2008) Verma (2013) and Vanave *et al.* (2014).

Panwar *et al.* (2008) conducted stability analysis for scented rice, under pooled analysis of variance, of genotype x environment interaction. They reported significant genotype x environment interaction for grain yield.

Hamam and Khaled (2009) field experiment conducted for stability analysis in wheat genotypes. The combined analysis of variance revealed highly significant differences between genotypes, sowing dates, nitrogen fertilizer levels, years and locations for all studied traits. They also suggest that days to heading, plant height, spike length, 1000-kernel weight, biomass and grain yield were significantly influenced by years, nitrogen fertilizer levels and genotypes. These results indicated that studied genotypes responded differently to the different environmental conditions

suggesting the importance of the assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment.

Koli and Chandra (2012) studied stability under stress condition and identified stable genotype based on regression coefficient.

Dewi *et al.* (2014) yield stability and adaptability of yield performance were analyzed by using coefficient regression (bi), general mean of yield and deviation of regression by Finlay-Wilkinson and Eberhart-Russell method and other parameters of stability and AMMI model. The combine analysis of variance revealed highly significant differences for grain yield among environment and genotype x environment interaction, while among genotype was significant, indicated differential performances of genotypes over environments. These results are supported by data mean square of E, G, and GEI were accounted significant for 19.641, 1.640, and 1.688 respectively. The significant and relatively large percentage of the total variation attributable to G x E interaction suggests that genotypes responded differentially to environment for rice grain yield.

Akter *et al.* (2015) studied genotype × environment interaction and yield stability analysis in hybrid rice. Data revealed that genotype (G), environment (E) and genotype × environment interaction (GEI) were highly significant ($P < 0.001$) for grain yield. The factors explained showed that rice grain yield was affected by genotype (48.61%), environment (19.98%) and their interaction (20.65%). Similar finding were also reported by (Shantha *et al.*, 2007; Samrat *et al.*, 2010; Mosavi *et al.*, 2013; Kota *et al.*, 2013).

2.7 Quality parameters

Murthy and Arunachalam (1966) stated that genetic drift and selection in environment could cause greater diversity than geographic distances. Considering this, parents should be selected on the basis of genetic diversity rather than geographic diversity which are supported by the findings of Hassan *et al.* (2000). Grouping of materials of similar origin into different clusters was an indication of broad genetic

base of the genotypes belonging to that origin. So genotypes originating from same place may have different genetic architecture or *vice versa* (Shanmugam and Rangaswamy, 1982).

Khatun *et al.* (2003) was reported that kernel breadth showed highly significant but negative correlation with L/B ratio.

Hossain *et al.* (2003) suggested that choosing of genotypes belonging to distant clusters was expected to execute maximum heterosis in crossing and to be used in hybridization program for obtaining a wide spectrum of variation among the segregants.

Babu *et al.* (2006) studied genetic divergence for different grain quality traits in 70 rice genotypes from different eco-geographical regions of India. The genotypes were grouped into nine clusters. Water uptake, gel consistency and head rice recovery contributed the maximum towards genetic divergence. Geographical diversity was not related with genetic diversity.

Roy *et al.* (2007) evaluated genetic divergence in twenty eight rice genotypes using D^2 statistics. These genotypes were grouped into four clusters. Seed yield per plant contributed the maximum towards genetic divergence followed by amylose content, cooked kernel length and thousand seed weight.

Sarkar *et al.* (2007) evaluated 41 genotypes of rice for ten different quality parameters of grains to assess the genetic variability and revealed that genotypic and phenotypic coefficient of variations were maximum for cooked kernel L/B ratio and 1000-grain weight.

Singh and Singh (2007) analyzed various cooking and physical qualities of rice. The hulling varied from 68.9 to 82.9%, milling from 56.1 to 74.2%, head rice recovery from 19.7 to 49.4%, kernel length (KL, uncooked) from 5.1 to 7.1 mm, kernel breadth (KB, uncooked) from 1.7 to 2.4 mm, kernel length breadth ratio from 2.31 to 3.94, KL (cooked) from 9.5 to 12.7 mm, KB (cooked) from 2.5 to 3.6 mm, kernel elongation ratio from 1.39 to 1.98, alkali score from 2.6 to 6.6 and water uptake from 390 to 500.

Gnanasekaran *et al.* (2008) reported positive correlation between grain yield and length-breadth ratio. Kernel length and Kernel breadth respectively had positive and negative correlations with length-breadth ratio.

Sharma *et al.* (2008) studied under irrigated situation using D^2 statistics in a set of 100 aromatic rice genotypes. The genotypes were grouped into nine clusters and it was observed that there was no association between the geographical distribution and genetic diversity.

Subudhi *et al.* (2009) also proposed to choose diverse parents for quality traits such as HRR, KLAC, GC, ER and AC from the most divergent clusters so that they produce larger variability and desirable segregants that would be productive in rice breeding program. The clustering pattern across locations showed that genotypes collected from the same geographic origin were found to be distributed in different clusters. Similar findings of non correspondence of genetic divergence with geographic diversity were reported earlier in rice by Murthy and Arunachalam (1966) and Rajesh *et al.* (2010).

Bajpai and Singh (2010) studied the grain quality of some short and medium grain aromatic rice and compared with premium Dehradun basmati 3020. The quality characteristics studied from consumer's point of view revealed that paddy length ranged from 6.8 mm to 7.4 mm. Kernel length ranged from 9.3 mm to 11.0 mm, elongation ratio ranged from 1.86 to 2.34, amylose content recorded was from 20.6 % to 25.5 %. The gelatinizing temperature was low in all lines except 3047 (intermediate) while aroma was strong in all lines except 3047, which revealed moderate aroma. The parameters studied from farmers/traders point of view revealed that hulling percentage ranged from 78.6 % to 81.6, milling percentage ranged from 72 % to 75 % while panicle length recorded ranged from 24.2 cm to 31.0 cm. From consumers point of view expect paddy length and kernel elongation all quality parameters of these line were near to premium Dehradun basmati 3020.

Shilpa *et al.* (2010) studied 22 traditionally cultivated rice varieties from Goa for physicochemical characteristics such as physical (hulling, head rice recovery, broken rice, grain classification, chalkiness) and cooking characteristics (elongation

ratio, water uptake). The hulling percentage ranged from 63-81% and head rice recovery from 45-74%. Among the varieties Length/Breath ratio ranged from 1.5-3.5 and the amylose content ranged from 14-25%. The kernel elongation ratio ranged from 4.78-1.83 mm and water uptake ratio ranged from 160-390.

Makwana *et al.* (2010) studied path analysis for qualitative and quantitative characters in slender grain rice. The analysis for quality components revealed that kernel length after cooking, showed high direct effects of kernel length and kernel elongation ratio; whereas selection for kernel L/B ratio, water uptake, alkali score (gelatinization temperature) and cooking time can indirectly improve the cooking quality.

Danbaba *et al.* (2011) studied on the cooking and eating quality of *Ofada* rice. The result showed that *Ofada* rice had high cooked rice volume with length and breadth increase of 152.54% and 87.85% respectively. Grain elongation ratio ranged from 1.24-1.75 and highest length/breadth ratio of cooked rice (3.68) and lowest (2.49) was recorded. Water uptake ratio, cooking time, solids in cooking gruel and amylase content of *Ofada* rice samples ranged from 174.0-211.0, 17-24 min, 0.8-2.1%, and 19.77-24.13% respectively.

Ekka *et al.* (2011) on the basis of association analysis reported that grain yield per plant had positive significant correlation with leaf width, days to 50 % flowering, plant height, panicle length, number of filled grains per panicle, 100 seed weight and paddy (grain) length. A positive and significant correlation of head rice recovery percentage was also observed with leaf length, leaf width, days to 50 % flowering, number of filled grains per panicle, spikelet sterility % and milling %.

Marschner (2012) and Zou *et al.* (2001) argued that the in most agricultural soils nitrate (NO_3^-) and ammoniums (NH_4^+) are the most abundant inorganic N forms. Besides serving as N source, these two N forms do also distinctly affect many physiological processes such as changes in rhizosphere pH or in the synthesis of organic acids which, in turn, may act as micronutrient chelators.

Barunawati *et al.* (2013) studied two-Way ANOVA and revealed that not only the N fertilization and the leaf developmental stage, but also their interactions had

significant effects on the micronutrients. The contents of Fe, Zn and Cu increased as grains matured. Importantly, the supply of a primarily ammonium-based fertilizer stimulated this increase only in mature but not in immature grains. Compared to non-fertilized and nitrate-supplied plants, the ammonium-based fertilization increased Fe contents in grains by almost 40% and those of Zn and Cu by 27 and 22% respectively similar result was also reported by Carlisle *et al.* (2012).

Parikh *et al.* (2012) evaluated physio-chemical characters and cooking quality of 36 rice genotypes and reported that the fine grain genotypes like Rajim-12, Kalimuchh, and Munibhog were good for moderate kernel length and L:B ratio; Rajabhog, Jhulari, and Baghmuchha for kernel length after cooking and L:B ratio of cooked rice Kalajira and Bikoni for head rice recovery %; Barang, Bantaphool, Gangabalu, and Bikoni for elongation ratio; Barang, Rajabhog, Gangabalu, Bikoni, and Chirainikhi for elongation index; Sonth, Rajim-12, Jhulari, Gangabalu, Jhilli Safri, and Bikoni for intermediate alkali values. These genotypes may be utilized as donors for improvement of quality traits.

Sarawgi *et al.* (2012) characterized 46 aromatic rice accessions of Dubraj group from Chhattisgarh and Madhya Pradesh for twenty morphological, six agronomical and eight quality characters. The specific accessions D: 1137, D: 812, D: 950, D: 959, D: 925, D: 1008, D: 939, D: 666I and D: 1090 were identified for quality and agronomical characteristics. These may be used in hybridization programme to achieve desired segregants for good grain quality with higher yield.

Satheeshkumar and Saravanan (2012) studied genetic diversity among fifty three genotypes of rice genotypes from various states of south Eastern region of India was evaluated using Mahalanobis D^2 statistic. Based on 15 morphological and quality characters, these genotypes were grouped into six Clusters. Geographical origin was not found to be a good parameter of genetic divergence.

Subudhi *et al.* (2012) evaluated forty-one rice varieties of different ecologies at CRRI, Cuttack and found that hulling percentage in all the genotypes ranged from 71.0 to 81.0, milling recovery varied from 62.0 to 76.0 and head rice recovery % varied from 43.5 to 68.0. The kernel length was highest (7.54) and lowest (3.88),

kernel length after cooking varied from 7.9 to 12.5, elongation ratio was highest (2.07) and (2.0) and lowest (1.44). Volume expansion ratio was 29 highest (5.25), and lowest (3.25).

Kumari *et al.* (2013) evaluated twelve accessions of rice for physical and biochemical traits and observed highest kernel length in NDR 6265 (7.07 mm) and kernel breadth in NDR 625 (1.81 mm). Maximum elongation ratio was observed in Kankjeer and Banta Phool A (1.88 mm) and kernel length after cooking was maximum in NDR 6265(11.4 mm). Maximum amylose content was found in variety Kalanamak Berdpur (19.8 %). On the basis of above parameters variety Kalanamak Berdpur, Badshah pasonda, NDR 6265 and NDR 625 were rated superior among the all varieties/accessions tested in the present investigation.

Phenotyping of the 41 rice genotypes was done by Pachauri *et al.* (2013) for grain quality characters viz., grain length, grain breadth, length breadth ratio, elongation ratio, alkali spreading value and aroma. The longest grain length (unmilled and milled) was recorded as 11.67 ± 0.4 mm and 8.2 ± 0.38 mm respectively for SS20, while Sulendas had shortest grain length of 6.93 ± 0.37 mm and 5.07 ± 0.15 mm respectively. Diverse L: B ratio (unmilled grain) was observed, ranging from 2.29 ± 0.24 mm (Suranit) to 5.66 ± 0.22 mm (SS20). Highest kernel elongation ratio was observed in Kakeria-2 (1.608 ± 0.19), while SHPP-20 showed the lowest elongation ratio of 1.078 ± 0.06 .

Vanisree *et al.* (2013) investigated fifty genotypes comprising both basmati and aromatic short grain types and revealed significant differences among genotypes for yield, its components and grain quality traits. The high variability was observed for productive tillers per plant and filled grain per panicle whereas, the estimates for panicle length, days to 50 % flowering, kernel breadth and kernel elongation ratio were low.

Allam *et al.* (2015) reported that Kernel L/B ratio showed positive and significant correlation with KLAC ($r_p=0.5510$, $r_g=0.5790$) and showed negative and significant correlation with elongation ratio ($r_p=-0.4235$, $r_g=-0.4397$). The study suggested that days to maturity, effective panicles, spikelets per panicle, spikelet

fertility, test weight, kernel length, kernel L/B ratio, KLAC, elongation ratio are important traits which should be used as selection criteria to develop high yielding and better quality varieties in basmati rice.

Devi *et al.* (2015a) studied genetic diversity in grain quality among 92 rice cultivars was evaluated using Mahalanobis D^2 statistic. Based on cluster analysis, the genotypes were grouped into 10 clusters of which clusters VII and IX are the largest clusters consisting of 16 genotypes each while cluster V was the smallest with only a single genotype. The maximum intra cluster distance ($D = 14066.5$) was found in cluster VI consisting of two traditional varieties AS 100 and Chittimutyalu. The most divergent clusters found were Clusters V and VI. Minimum inter cluster distance ($D = 5144.43$) was found between Clusters VIII and IX. Kernel breadth (0.01%), volume expansion ratio (0.39 %) and elongation ratio (0.30%) failed to contribute significantly towards genetic diversity. Amylose content (25.2%), gel consistency (20.4 %), 1000 grain weight (12.6 %) and head rice recovery (10.1%) were found to be the most contributing traits towards genetic diversity. Hence these traits could be focused for selection while improving grain quality.

Devi *et al.* (2015b) ninety-two rice (*Oryza sativa L.*) genotypes were evaluated during kharif 2013 to estimate the correlation coefficients for 14 physicochemical and cooking quality traits. The study revealed that, significant and positive correlation of KLAC with ER ($r = 0.638$) and L/B ratio ($r = 0.556$), ASV with water uptake ($r = 0.426$), hulling % with milling % ($r = 0.60$) and with HRR % ($r = 0.150$) indicated that these are the primary traits for improvement of rice grain quality.

Gangadharaiah *et al.* (2015) studied the physicochemical and cooking quality of traditional rice cultivars grown in the farmer's field. Among the cultivars, Kichadi Sona and Salem Sanna recorded higher milling yield (66.0% and 65.0%) and head rice recovery (58.5% and 58.30%), respectively. Therefore, these cultivars could be utilized in the breeding programme is the need of the today towards the "hidden hunger" free world.

Hosen *et al.* (2016) studied 17 Aus rice cultivars including 10 local cultivars. The highest milling outturn 72.22% was found in the traditional variety Chakilla and

lowest in Kasalath (65.43%). The highest milled rice length (6.5 mm) was BRRI dhan 42 and the highest length-breadth ratio (3.8) was found in both BR24 and BR26. The lowest grain length was found in BR20 (5.0 mm) and lowest length-breadth ratio was found in Phul Dumra (2.0). In addition, Surjamukhi has aroma. These local Aus variety could be a useful germplasm in breeding program to get improve HYV especially for Aus season.

2.8 Molecular markers and diversity analysis

The first restriction fragment length polymorphism (RFLP) map of rice was constructed in the 1980s at Cornell University (McCouch *et al.*, 1988).

There are many types of DNA markers that are produced by a wide variety of techniques (Mohan *et al.*, 1997) yet only a subset has been widely used for whole genome mapping projects. RFLPs, RAPDs, AFLP, simple sequence repeat (SSR) and more recently SNP are the most popular molecular markers used in genome mapping. DNA markers are employed to construct the genetic map of organism, to map the genes governing qualitative and quantitative traits, to exercise indirect selection for various agronomic traits and to isolate the gene based on map position.

The higher density of SSR markers was found on chromosome #1, #3 and #5 (with 5.6, 5.8 and 5.6 SSRs per Mb, respectively) and the lower density was observed on chromosomes #8, #9, #10, #11 and #12 (McCouch *et al.*, 2002).

In rice more than 2500 microsatellite markers have been developed and used to construct genetic map (McCouch *et al.*, 2002). Singh *et al.* (2009) developed 436 HvSSR markers which are evenly distributed in the rice genome.

Srividhya *et al.* (2011) used 412 rice microsatellite primers to screen the parents, 113 found to be polymorphic and they are used these polymorphic marker for Construction of Linkage Map and QTL Mapping.

Bhoopathi *et al.* (2011) used 34 SSR markers mapped in the vicinity of RM28048 and RM511 were selected for BSA analysis.

Karmakar *et al.* (2012) studied landraces were genotyped with 22 reported SSR markers mapped within osmotic stress tolerance linked QTL loci from four different chromosomes.

Suji *et al.* (2012) used flanking SSR markers, RM252–RM348 and RM348–RM280 for basal root thickness and root pulling force QTLs on chromosome 4 and RM257–RM242 for penetrated root thickness QTL on chromosome 9 and these were used in foreground selection of backcross progenies.

Martin *et al.* (2012) study was undertaken to assess the genetic diversity among deep water rice genotypes using Simple Sequence Repeat (SSR) markers through marker aided selection (MAS). The polymorphism information content (PIC) reflections of alleles diversity frequency among the varieties, which is ranged from 0.477 to 0.782, with an average of 0.634. The Unweighted Pair Group Method with Arithmetic Mean (UPGMA) dendrogram revealed 2 major groups with 4 clusters and the wide range of dissimilarity values (0.14-0.89) which showed a high degree of diversity among the cultivars. Similar results were also reported by Garriss *et al.* (2005) and Thomson *et al.* (2007).

The SSR markers have been used widely for rice germplasm evaluation, interpreting population structure and dissection of quantitative trait loci (QTLs) for important agronomic traits (Akkaya *et al.*, 1992; Yang *et al.*, 1994; McCouch *et al.*, 1997, 2002; Cho *et al.*, 2000; Singh *et al.*, 2013).

Wang *et al.* (2013) prepared linkage map for the RILs, which comprised 198 simple sequence repeat (SSR) markers, spanned 1814.5 cM, with an average spacing of 9.2 cM between adjacent markers.

The five SSR markers viz., RM202, RM212, RM258, RM264 and RM279 were found polymorphic among the 66 SSR markers screened between parents (Mahamaya × Budda) by Prakash *et al.* (2015).

2.9 Identification of quantitative trait loci for grain yield and its components

The principles of QTL analysis were first outlined and successfully applied in the early 1920s to map a QTL for seed size which tightly linked to a gene controlling seed pigmentation (Sax, 1923).

The time consuming process of map construction was considerably shortened with the introduction of the PCR based microsatellite (SSR, simple sequence repeat) markers, particularly suited for mapping purposes due to their high level of polymorphism (Taramino and Tingey, 1996).

There are several statistical methods developed to analyze mapping data to search systematically for major QTLs in experimental organisms. The traditional method known as single marker analysis or point analysis is used to detect association between a QTL and a marker. Thoday (1961) and Soller and Brody (1976) described the idea of using single genetic markers one at a time to systematically characterize and map individual polygene's controlling the quantitative trait. For detecting a QTL near a marker, phenotypic means for the progeny of each marker class are compared (Edwards *et al.*, 1987).

There are three widely used methods for detecting QTLs, single marker analysis, simple interval mapping and composite interval mapping (Tanksley, 1993). Single marker approach, sometime referred to as the single factor analysis of variance (SF-ANOVA) or simple point analysis, is the simplest method for detecting QTLs associated with single markers. SF-ANOVA is done for each marker locus independent of information from other loci. F-test provides evidence whether differences between marker locus genotype classes are significant or not. The statistical methods used for single-marker analysis include t-test, analysis of variance (ANOVA) and linear regression. Linear regression is most commonly used because the coefficient of determination (R^2) from the marker explains the phenotypic variation arising from QTL linked to the marker. This method does not require a linkage map and can be performed with basic statistical software programs. However,

the major disadvantage with this method is that the further a QTL is from a marker, the less likely it will be detected. This is because recombination may occur between the marker and the QTL. This causes the magnitude of the effect of a QTL to be underestimated (Tanksley, 1993). Q-Gene and MapManager QTX are commonly used computer programmes to perform single-marker analysis (Nelson, 1997)

Different software was developed for QTL analysis *viz.*, MAPMAKER/ QTL (Lincoln *et al.*, 1992), QTL cartographer (Basten *et al.*, 1997), Map Manager QT (Manly and Elliott, 1991), MQTL (Tinker and Mather, 1995), QTL Network (Yang *et al.*, 2007) and QTL IciMapping (Li *et al.*, 2007).

Venuprasad *et al.* (2001) worked on IR64 X Azucena DH mapping population of rice in three diverse environments and detected QTLs for ten traits at a threshold. The QTLs were spread across six chromosomes 1, 3, 4, 5, 6, and 7. Three QTLs for grain yield were detected one each on chromosome 3, 4 and 5.

Wang *et al.* (2003) identified several QILs related to panicle number and grain yield in field experiments under normal N fertilization and low N-treatments. Wei *et al.* (2011) detected QTLs for rice NUE and grain yield traits, and studied the genetic relationship between the two traits. They identified 68 QTLs for grain yield and its components under the low and normal N applications.

QTLs for yield and yield components, panicle sterility etc in rice was identified (Jonaliza *et al.*, 2004) in RIL population of a cross between CT9993 and IR62266. Xu *et al.* (2005) identified 36 QTLs in introgression indica lines of rice for yield and its components under drought.

Babu *et al.* (2003) reported 47 QTLs for leaf rolling and drying scores, days to heading (days after sowing), plant height, grain yield, biomass, spikelet fertility, seeds per panicle, harvest index and relative yield by interval mapping *via*. QTL Mapper version 1.0 in a doubled-haploid rice population of 154 lines from CT9993 and IR62266 in different trials.

Lafitte *et al.* (2004b) identified 31 QTLs for yield and its components in rice under drought working with RIL population of Bala × Azucena.

Lanceras *et al.* (2004) used RIL population of a cross between CT9993 and IR62266, and identified 77 QTLs for yield; yield components, panicle sterility etc. in rice.

Verulker *et al.* (2004) identified 143 QTLs for various traits in rice.

Ashikari *et al.* (2005) identified a major QTL for grain number (*Gn1*) and a QTL for plant height (*Ph1*) by using the progeny from the cross between japonica rice, Koshihikari, and indica rice, Habataki.

Xiao *et al.* (2005) reported identification of 2, 4, 4, 1, 2, 2 and 3 QTLs for grain yield, 100 kernel weight, kernel number per ear, cob weight per ear, kernel weight per ear, ear weight and ear number per plant respectively under well-watered regime and 1, 5, 2, 6, 1, 3 and 2 QTLs respectively under water-stress condition.

QTLs for grain yield and its component traits (e.g., spikelet fertility, spikelet number per panicle, 1000-grain weight, and panicle number) were identified by Zou *et al.* (2005).

Tong (2006) identified 31 QTLs that controls plant height, the number of panicles per plant, chlorophyll content, shoot dry weight and grain yield per plant, using a population of chromosome segment substitution lines at the late developmental stage under two N conditions.

Yue *et al.* (2006) reported 39 QTLs for productivity, spikelet fertility, leaf rolling, biomass, harvest index and grain weight with RIL population of *indica* lowland × tropical *japonica* upland.

Bernier *et al.* (2007) used population of 436 random F3 derived line from a cross between the upland rice cultivar Vandana and Way Rarem, and reported *qtl12.1* on chromosome 12 with large effect on grain yield under stress. They also reported that under stress also increases harvest index, biomass yield and plant height while reducing the number of days to flowering.

Cho *et al.* (2007) conducted study to identify QTLs for traits associated with physiological nitrogen use efficiency (PNUE). PNUE was positively correlated with the harvest index and grain yield under ordinary low-nitrogen and high-nitrogen conditions. Twenty single QTLs (S-QTLs) and 58 pairs of epistatic loci (E-QTLs)

were identified for the nitrogen concentration of grain, nitrogen concentration of straw, nitrogen content of shoot, harvest index, grain yield, straw yield and PNUE in both conditions.

Panicle length-associated QTLs, panicle number-associated QTLs, and spikelet number per panicle-associated QTLs were mapped in RM17169-RM17183, RM5320-RM17355, and RM5320- RM17355, respectively, within the target region RM273- RM255 on chromosome 4 via molecular marker by Liu (2010).

Cui *et al.* (2008) reported 34 QTLs for plant height, maximum root length etc. by using Zhenshan 97 × Minghui 63 population. Some QTLs associated with root traits that increase yield in upland rice have been investigated (Steele *et al.*, 2013).

Three main-effect QTLs related to panicle length, panicle number, and spikelet number per panicle were identified in the target interval of RM273-RM255 on chromosome 4 (Nie *et al.*, 2015). The panicle length-related QTL had two loci located in the neighboring intervals of RM17308-RM17305 and RM17349- RM17190, which explained 18.80% and 20.42%, respectively, of the phenotypic variation, while the panicle number-related QTL was identified in the interval of RM1354-RM17308, explaining 11.47% of the phenotypic variation. As far as the spikelet number per panicle-related QTL was concerned, it was found to be located in the interval of RM17308-RM17305, which explained 28.08% of the phenotypic variation.

CHAPTER - III

MATERIALS AND METHODS

The present study entitled “**Genetical studies on NO₃⁻ use efficiency under aerobic and anaerobic conditions in rice (*Oryza sativa* L.)**” was conducted at the Research cum Instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), during wet season 2015 and 2016 to generate the phenotypic data under managed field conditions. The material used, techniques adopted and statistical tools that have helped in interpreting the data are briefly presented in this chapter.

3.1 Experimental site

The present research work was conducted at Research cum Instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, during the *Kharif* season of 2015 and 2016. Raipur is situated in mid-eastern part of Chhattisgarh state and lies at 21° 16' N latitude and 81° 36' E longitudes with an altitude of 298.56 meter above the mean sea level.

3.2 Physio-chemical characteristics of soil of the experimental field

The experimental soil (Vertisol) is fine montmorillonite. It is usually deep, heavy, clayey, dark brown to black in colour and neutral. Soil from experimental fields was analyzed for its initial characteristics and some important physio-chemical properties of the soil are given in Table 3.1.

3.3 Climatic and weather conditions

The region comes under dry and sub-humid climate. Weekly rainfall pattern, maximum and minimum temperature for the wet cropping season *kharif*-2015 and *Kharif*-2016 were recorded throughout the growing season (Appendices- A and B).

Table: 3.1 Physio-chemical properties of the soil from the experimental field

Physio-chemical properties	Values			
	2015		2016	
	Anaerobic	Aerobic	Anaerobic	Aerobic
a) pH	6.9	6.5	7.0	6.8
b) EC(dsm ⁻¹)	0.15	0.14	0.18	0.16
c) Organic carbon (%)	0.59	0.34	0.60	0.31
d) N (kg/ha)	150.5	112.9	162.6	118.6
e) P (kg/ha)	18.73	9.23	17.34	12.3
f) K (kg/ha)	603.5	481.1	588.7	465.7
g) Fe (ppm)	25.7	24.9	26.8	22.9
h) Zn (ppm)	1.08	1.28	1.18	1.32

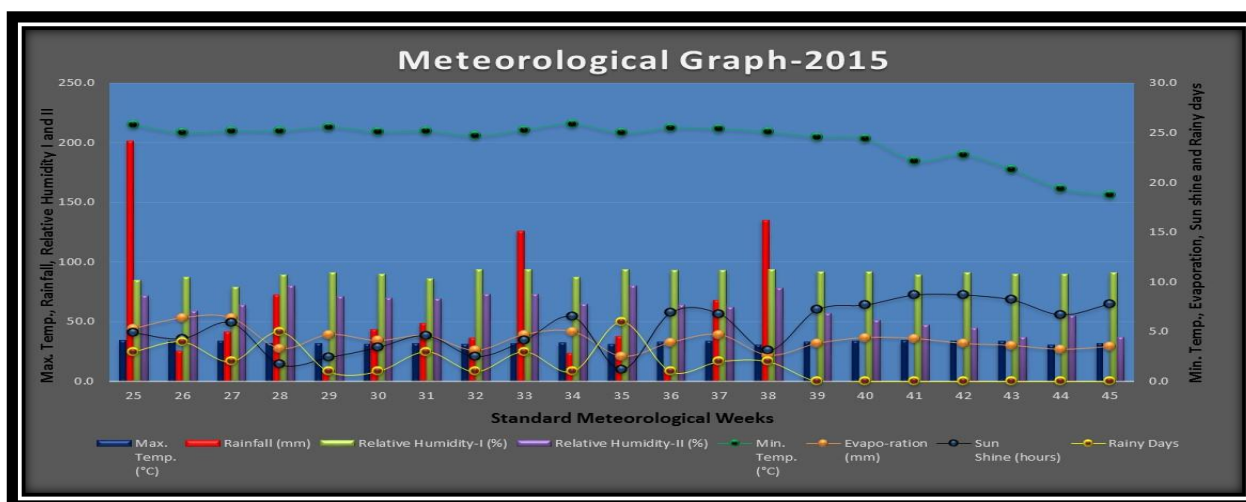


Fig. 3.1(a) Maximum, minimum temperature and rainfall during the field evaluation of study material (wet season 2015)

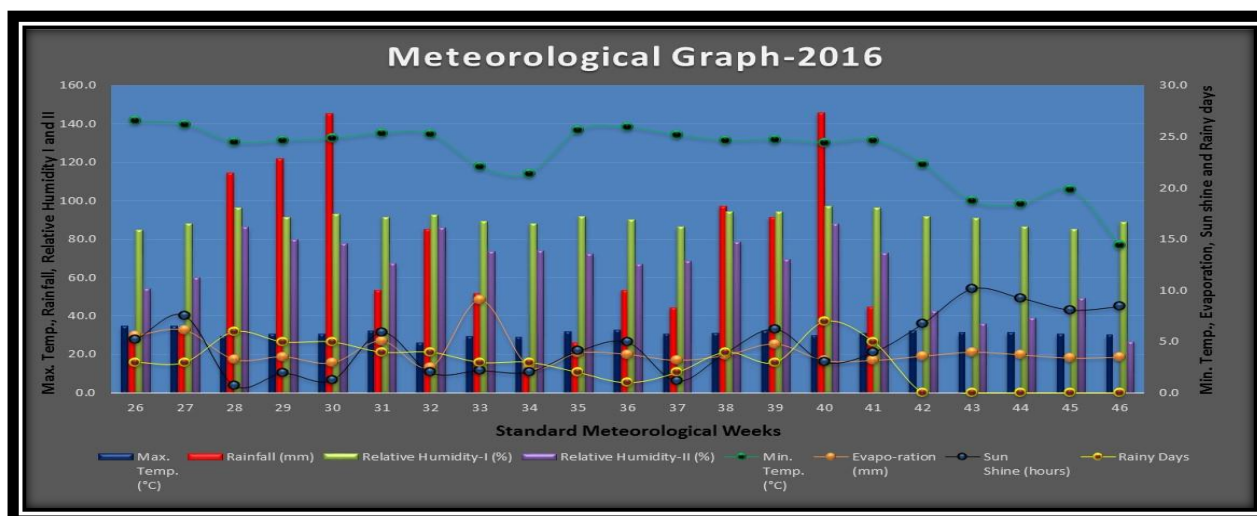


Fig. 3.1(b) Maximum, minimum temperature and rainfall during the field evaluation of study material (wet season 2016)

The total rainfall during crop cycle for wet season 2015 was 880.6 mm and wet season 2016 was 1152.8 mm as shown in Fig. 3.1 (a) and Fig. 3.1 (b).

3.4 Materials

The material in present study includes two sets, in first set 123 rice lines including released varieties, advanced breeding lines, land races and 7 checks (CH). List of genotypes under study is given in Table 3.2.

Table: 3.2 List of genotypes used under study

Sr. No.	Name of Entry	Sr. No.	Name of Entry	Sr. No.	Name of Entry
CH-1	Indira Sona	34	CR 3632-1-2	79	R 1532-1244-3-1109-1
CH-2	Indira Aerobic 1	35	CR 3634-1-3	80	Badshahbhog
CH-3	Swarna	41	Anjali	81	Dubraj
CH-4	Basmati- 370	42	Neha	82	Vishnubhog
CH-5	IR-64 Drought	43	CR Dhan 40	83	Bargi
CH-6	Samleshwari	44	Poornima	84	Anjan I
CH-7	Danteshwari	45	R 2212-RF-75	85	Badshah Bhog II
1	RP 5125-2-4	46	R 1033-968-2-1	86	Jogi Bhog
2	R 1779-321-1-112-1	47	R 1744-4901-1-1-510-1	87	Anjan II
3	R 1882-306-4-243-1	48	R-RHZ-2	88	Anjan (CGR-1814)
4	R 1892-486-1-151-1	49	R-RF 105	89	Anjan (CGR-1817)
5	BP 10620 F-BB 4-13-BB 8	50	R 1670-3269-2-3926-1	90	Anjan (CGR-1818)
6	IR 76939-98-1-1-1	51	R 1678-1901-1-1473-1	91	Anjaniya
7	R 1674-1823-2-1189-1	52	R 1902-912-2-512-1	92	Lal Banko
8	R 1973-206-2-86-1	53	R 1695-270-2-133-1	93	Mudi Banko
9	CB 07-103	54	MTU 1010	94	Raj Banko
10	IR 79538-1-1-1-1	55	R 1598-483-1-297-1	95	Byarangi
11	R 2093-1536-1-660-1	56	R 1570-2649-1-1546-1	96	Barangi
12	R 1630-1237-2-827-1	57	R 1670-3975-1-485-1	97	Urai Buta I
13	Ganjeikalli	58	R 1570-2644-2-1547-1	98	Urai Buta II
14	R 1630-33-1-23-1	59	IGKVR 1	99	Ilayachi I
15	CR 2713-11	60	R 1702-3677-1-4734-1	100	Mauhakuchi
16	IR 84887-B-15	61	R 741-1-55-2-1-R-1	101	Rajniti (A)
17	R 1700-308-3-170-1	62	Chandrasini	102	Digamber Dhan
18	IR 83376-B-B-110-3	63	R-RHZ-LI-22	103	Dadhmaini Dhan
19	R 1917-951-1-541-1	64	R 1432-251-103-1-1	104	Chhota Dhan
20	R 1700-309-1-171-1	65	IGKVR 1244	105	Safed Lalak
21	R 1672-1171-1-124-1	66	Mahamaya	106	Sitasaal Dhan
22	R 1695-133-1-72-1	67	Bamleshwari	107	Tewan Dhan
23	R 1262-1667-1-1	68	R 1700-2243-2-2312-1	108	Mehardhan-1
24	R 1860-783-1-424-1	69	R 1641-391-1-61-1	109	Kendumudi-1
25	R 1670-3269-2-3926-1	70	R 1641-914-1-400-1	110	Bhajna
26	BRR-0006	71	IGKVR 2	111	Dadbako
27	RAU 1484-Aer-04	72	R 1641-907-1-397-1	112	CR Dhan 201
28	RCPR 8	73	R 304-34-R-1	113	CR Dhan 202
29	RCPR 6	74	R 1138-688-3-533-1	114	IR-64
30	BRR-0007	75	R 1536-136-1-77-1	115	Indira Barani Dhan 1
31	R 1240-913-2-1013-1	76	R 1747-4941-1-515-1	116	Sampada
32	CR-3631-1-3	77	R 1656-1146-5-513-1		
33	CB 09 512	78	R 1521-950-6-843-1		

In another set Swarna and Basmati-370 and their 179 recombinant inbred lines (RILs) population were used. The recombinant inbred lines (RILs) were developed by using modified single seed descent method (SSD) to F8, F9 generation. Lines were selected based on yield and yield contributing parameters for further study. Characteristics features of parent are given in Table 3.3.

Table: 3.3 Characteristic features of parent of RILs

S. No.	Parent	Pedigree	Salient Features
1	Swarna	Vasista × Mahsuri	High yielding, Semi dwarf, Low nitrogen requirement, Maturity duration 145-150 days Grain Type: Medium slender
2	Basmati-370	Traditional Variety	Aromatic, Tall, Maturity duration 130-135 days Grain type: Long slender

3.5 Experimental details

During wet season 2015, the set of genotypes was evaluated under two field conditions *viz.*, anaerobic, aerobic and set of RILs was evaluated in aerobic condition due to lack of seed availability. The entire experiment was laid out with two different form of nitrogen *viz.*, NH_4^+ (in the form of Ammonium Chloride) and NO_3^- (in the form of Calcium Nitrate) along with N^0 (Control). Augmented design is useful under the situation when large number of entries is to be evaluated and sufficient land may not be available (Federer, 1956). The experiment was conducted in augmented design, the material under study was evaluated with five block and seven checks separately for three types of nitrogen regimes under both anaerobic and aerobic condition.

During wet season 2016, selected lines were evaluated in factorial randomized block design with two replication for different forms of nitrogen under varied sets of conditions. .The treatments employed for all sets of environments is depicted in Table 3.4.

Table: 3.4 Treatments for studying NH_4^+ and NO_3^- use efficiency wet season 2016

Levels of first factor	Fertilizer	Treatment
N1	Ammonium Chloride	NH_4^+ -N
N2	Calcium Nitrate	NO_3^- -N
N3	Control	N^0 -N
Levels of second factor	Environment/ field conditions	Soil moisture regime
E1	Irrigated/Anaerobic	Non-stress
E2	Rainfed/Aerobic	Stress

3.6. Sowing and Cultural practices

3.6.1. Raising the seedling and transplanting

Well pulverized raised nursery beds were prepared. The size of each nursery beds were 0.5 meter broad having 25 cm height. Drainage channel of 30 cm width was provided between the beds. The seeds were sown in the raised nursery bed by hand drilling methods in rows. Light and frequent irrigation were given until the seedlings were transplanted. Twenty five days old seedlings and single seedling per hill was transplanted in the field. The details of experiment during wet season 2015 and 2016 are given in Table 3.5 and field view shown in Fig. 3.2 and Fig. 3.3.

Table: 3.5 General information about sowing

Conditions	Date of sowing	Date of Trans-planting	Spacing (cm)		No. of row/line	Length of row (m)	Number of replication
			Row to row	Plant to plant			
Wet season -2015							
T/Anaerobic	26 June	21 July	20	15	3	2	Augmented Design
Ds/Aerobic	30 June	-	20	-	2	2	
Wet season -2016							
T/Anaerobic	30 June	25 July	20	15	2	1.8	2
Ds/Aerobic	29 June	-	20	-	2	1.8	2

Where, **Ds**=Direct seeded, **T**= Transplanted.

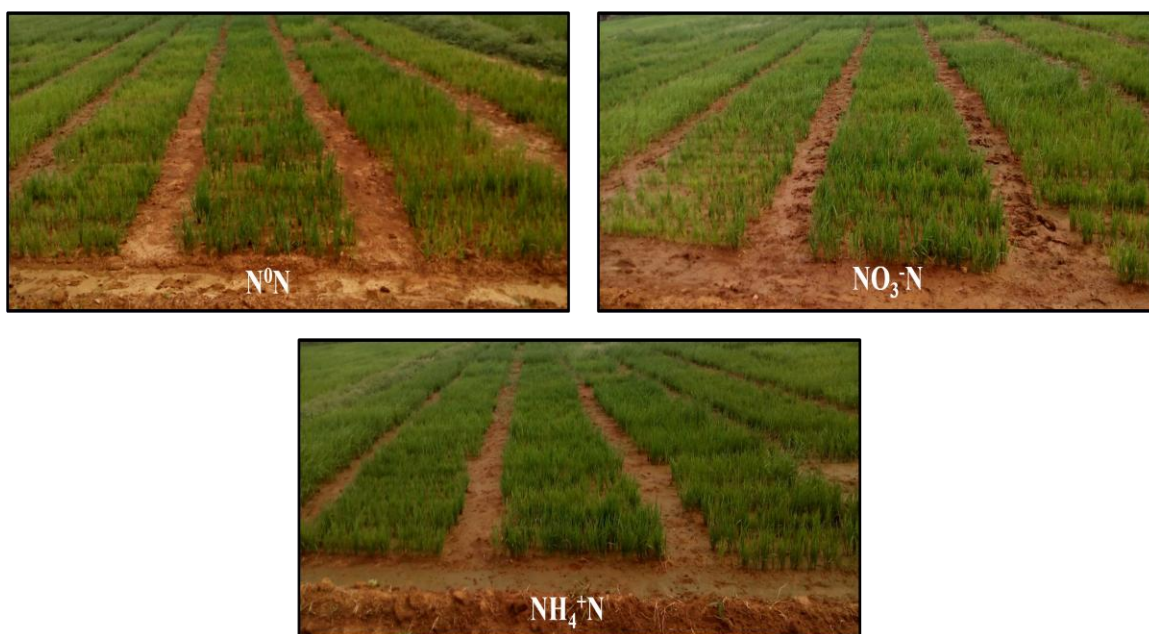


Fig. 3.2 General view of field experiment under NO_3^-N and NH_4^+N treatment for aerobic condition during wet season -2015

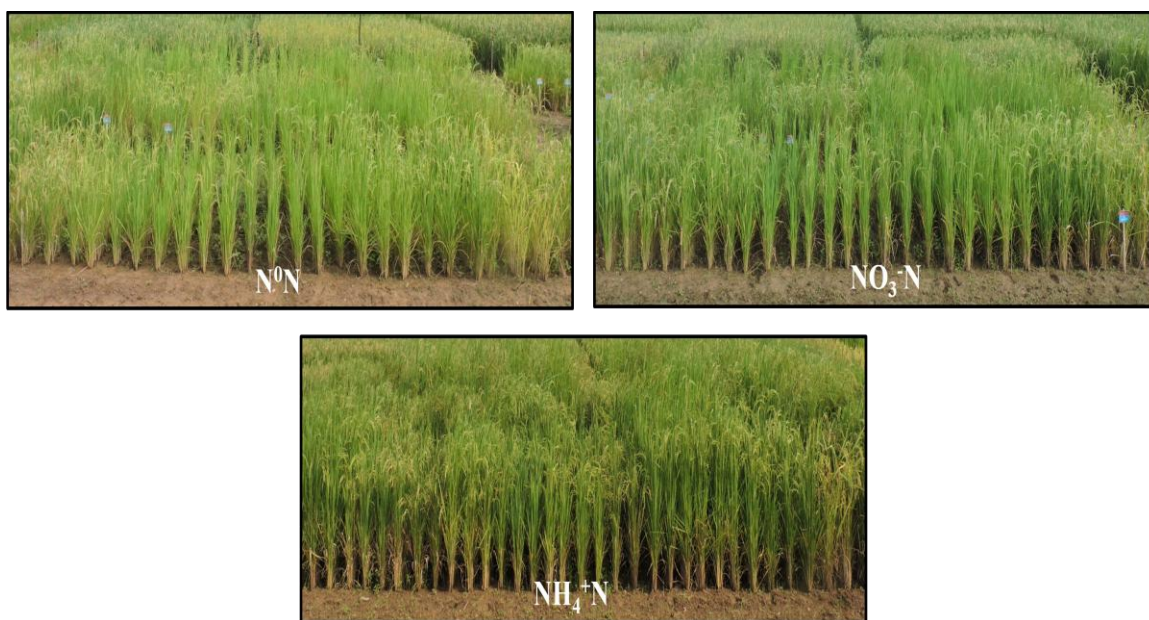


Fig. 3.3 General view of field experiment under NO_3^-N and NH_4^+N treatment for aerobic condition during wet season -2016

3.6.2. Field preparation

The final preparation of the field was done by two criss-cross tractor ploughing followed by harrowing. The soil surface was labelled and the field was divided for the respective treatments and replication. To limit seepage losses and movement of fertilizer, a well compacted bund was prepared and any cracks or rat holes was plastered with mud before application of treatments.

3.6.3. Fertilizer application

The fertilizers were applied as per the recommended package of practice. The ratio of 80:60:40 kg ha⁻¹ N: P: K was applied in the form of ammonium chloride/ calcium nitrate, single super phosphate and murate of potash, respectively. Nitrogen was applied in 3 splits, viz., 50% of the total N as basal dose, 25% at panicle initiation and the remaining 25% at flowering. The whole amount of phosphorus and potash was applied as basal.

The weeds were removed from the plot manually as per requirement; hand weeding was done at 20 days interval. After transplanting the soil was kept saturated until seedlings got established in transplanted field. After establishment of seedling standing water was maintained throughout the growing period.

3.7. Observations recorded under field conditions

To assess the effect of treatments on growth and development of crop plants, observations were recorded at plant specific stage during their maximum tillering stage, vegetative stage, maturation stage and some important post-harvest observations (quality traits), were also recorded according to SES (IRRI, 2002). The five randomly plants were selected from each entry and observations were recorded for morphological and physiological traits.

3.7.1 Quantitative Traits

3.7.1.1 Seedling height (cm)

Seedling height was measured in centimeter (cm), after 35 to 45 days under transplanted as well as direct seeded condition from soil surface to tip of the upper leaf.

3.7.1.2 Days to 50 % flowering

The time taken (days) from sowing to flowering period of half of the plants from each line were recorded on plot basis by visual means.

3.7.1.3 Plant height (cm)

Plant height of individual five selected plants was measured in centimeter (cm) from soil surface to tip of the tallest panicle at maturity using standard scaling method and averaged it.

3.7.1.4 Number of effective tillers per plant

Number of productive tiller of five selected plants was recorded under transplanted condition by counting number of tillers on which the panicle is emerged in each hill of plant at maturity stage and averaged it.

3.7.1.5 Panicle length (cm)

Panicle length of five selected plants was measured in centimeters (cm) from base to tip of panicle using standard scaling method.

3.7.1.6 Number of spikelet's per panicle

It is recorded by counting number of total grains in single panicle. Five panicles were used then averaged it.

3.7.1.7 Number of filled grain per panicle

It is recorded by counting the number of filled grains in single panicle. Five panicles were used then averaged it.

3.7.1.8 Biological yield (gm^{-2})

The biological yield was recorded as actual weight in gram of total biomass of shoot portion per plot and later converted to g/ m^2 for further analysis.

3.7.1.9 Grain yield (gm⁻²)

The actual yield of grain in gram per plot was recorded and later converted to g/ m² for further analysis.

3.7.1.10 Harvest index (%)

Harvest index was worked out by using the formula as given below:

$$HI (\%) = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.7.1.11 100 seeds weight (g)

100 seeds weight was recorded for each line in grams (g).

3.7.2 Physiological Traits

Leaf chlorophyll content was measured by *in vivo* procedure using Soil Plant Analysis Diagnostic Meter (SPAD-502, 1989 Minolta Co. Ltd.)

SPAD-502 was used to measure chlorophyll content of leaves in SPAD units. Leaf chlorophyll content was measured by light absorbance in the range of red and infrared with the chlorophyll meter in the middle region of fully open flag leaf and penultimate leaf of five representative plants. Readings were measured during seedling and flowering stages. Mean SPAD reading was recorded. SPAD reading is equivalent to chlorophyll content in g/cm².

3.7.3 Grain quality parameters

Following grain quality parameters were recorded on selected genotypes.

3.7.3.1 Hulling (%)

50 g of paddy sample was used; it was properly cleaned, before starting the dehulling. The dehulling of rice was done by dehusker and hulled rice weight was recorded.

$$\text{Hulling percentage} = \frac{\text{Weight of the dehusked kernel}}{\text{Weight of paddy}} \times 100$$

3.7.3.2 Milling (%)

Brown rice was put into standard miller or polisher and later milled rice weight was recorded.

$$\text{Milling percentage} = \frac{\text{Weight of polished kernel}}{\text{Weight of paddy}} \times 100$$

3.7.3.3 Head rice recovery (%)

From milled rice the $\frac{3}{4}$ kernel was taken as whole grain. The sorting out of full and broken rice was done and its weight was recorded.

$$\text{HRR (\%)} = \frac{\text{Weight of whole polished kernel}}{\text{Weight of paddy}} \times 100$$

3.7.3.4 Kernel length (mm)

Ten milled grains were taken randomly and average length was recorded in millimeters.

3.7.3.5 Kernel breadth (mm)

Breadth of the above ten milled grains was recorded and average breadth was recorded in millimeters.

3.7.3.6 L/B Ratio

The length/breadth ratio of randomly selected ten milled spikelets was calculated by dividing respective length with breadth.

$$\text{Kernel L/B ratio} = \frac{\text{Length of milled grains}}{\text{Breadth of milled grains}}$$

3.7.3.7 Kernal length after cooking (mm)

The length of randomly selected ten cooked grains was measured in terms of millimeters.

3.7.3.8 Kernel breadth after cooking (mm)

The breadth of randomly selected ten cooked grains were measured in terms of millimeters.

3.7.3.9 Length breadth ratio after cooking

The length/breadth ratio of randomly selected ten cooked grains was calculated by dividing respective length with breadth. It was computed by formula:

$$\text{Length breadth ratio after cooking} = \frac{\text{Kernel length after cooking}}{\text{Kernel breadth after cooking}}$$

3.7.3.10 Elongation Ratio

This was calculated by the following formula:

$$\text{Elongation ratio} = \frac{\text{Kernel length after cooking (mm)}}{\text{Kernel length before cooking (mm)}}$$

3.7.3.11 Elongation Index

Elongation index was calculated by the following formula:

$$\text{Elongation index} = \frac{\text{Ratio of L/B (after cooking)}}{\text{Ratio of L/B (before cooking)}}$$

3.7.3.12 Water uptake (ml)

(a) Material

1. Graduated test tube
2. Constant temperature water bath
3. Measuring cylinder

(b) Procedure

- Take 2 gm sample in a graduated test tube pour 10 ml of water or measure 10 ml water and put into ungraduated test tube, let it soak for 30 minute.
- Keep 2-3 test tubes with 10 ml of water as control along with the samples in the water bath.
- Then boil for 45 minute at 77° C to 80° C in a constant temperature water bath.
- Immediately place the tubes in a beaker containing cold water for cooling.
- Pour the supernant water into graduated cylinder after cooling and note the water level i.e. (a) water remaining after cooking (ml), (b) water absorbed during cooking (ml), (c) actual water absorbed (ml)=water absorbed during cooking-control (evaporated water).
- Then water uptake was calculated by the following formula.

Water Uptake (ml) = $100/2 \times$ Actual water absorbed.

3.7.3.13 Iron and Zinc content (mg/kg or ppm)

Iron and Zinc content from rice grain samples were estimated at IIRR, Hyderabad (former DRR) by using Energy dispersive X-Ray Fluorescence Spectrometry (XRF). In XRF the preselected wavelength of incident X-rays expel an electron from the innermost orbit followed by the transfer of one of the electrons from the outermost orbit to innermost orbit leading to release of specific wavelength of X-rays. The energy of the emitted radiation is specific for a particular atom. Therefore, it is simultaneously identified and quantified by the detector. This instrument is quite useful in non-destructive determination of relative iron and zinc concentrations in rice samples (Ravindra Babu, 2013).

3.8 Nitrogen estimation

At maturity, representative samples of straw were obtained from the central net plot area of each line. The samples were oven dried at 70 °C to a constant weight. The Steps are enumerated below:

3.8.1 Equipments required

- Weighing balance
- KEL plus digestion and distillation apparatus
- Kjeldahl flasks
- Micro Burette

3.8.2 Procedure

3.8.2.1. Processing of rice straw and grains

Before analyzing the rice grain samples were subjected to dehusking by dehusker and oven dry straw samples of respective lines were cut into small pieces using scissor for digestion.

3.8.2.2. Estimation of protein

Total protein content of brown rice grains of all samples was estimated by modified micro-Kjeldahl method. The details of the procedure are as under.

i) Digestion process

About 0.5 gm of rice grain/straw was transferred into the digestion tube and 3 gm of K_2SO_4 and $CuSO_4$ mixture was added (sample and K_2SO_4 & $CuSO_4 \cdot 5H_2O$ in the ratio of 1:10). 10 ml of concentrated Sulphuric acid was added and digestion tubes were placed on the digestion block with temperature set at 400 °C. After 2 to 3 hours when the samples colour turned light green, the digestion tubes were taken out of digestion block. The tubes were allowed to cool at room temperature.

ii) Distillation process

Digested samples were subjected to Pelican make distillation unit and distillation of samples was carried using 4% Boric acid and 40% Sodium hydroxide. 10 ml of Boric acid indicator was taken in conical flask. The flask was beneath the condenser with the delivery tip immersed in the solution. The digested samples were transferred to distillation apparatus and 35 ml of 40% sodium hydroxide was added to it. After 3 minute of processing time around 20 ml of green color distillate was collected in a conical flask. A blank was always run containing the same quantities of the entire reagent but without the sample for every set of nitrogen determination.

iii) Titration process

The distilled samples were titrated against the 0.05 N Sulfamic acid until the first appearance of violate colour as the end point. The titer value was used to calculate percent Nitrogen, which is then used to estimate total protein content by using conversion factor 5.95 (Julliano and Villareal, 1993).

$$\text{Nitrogen (\%)} = \frac{(\text{Vol. of sulphamic acid} - \text{Vol. of blank}) \times \text{Normality} \times 14 \times 100}{\text{Sample weight (gm)} \times 1000}$$

$$\text{Grain Protein content (\%)} = \% \text{ N} \times 5.95$$

3.8.2.3. Determination of Nitrogen use efficiencies and their related traits

Nitrogen use efficiency and their related traits were calculated by using the following formulas.

$$\text{a. Grain nitrogen yield (GNY)} = (\text{GNC} \times \text{GY})/100 \quad \text{g/m}^2$$

- | | | | | |
|-----------|--|---|------------------------------|------------|
| b. | Straw nitrogen yield (SNY) | = | $SNC \times (BY - GY) / 100$ | g/m^2 |
| c. | Biological nitrogen yield (BNY) | = | $GNY + SNY$ | g/m^2 |
| d. | Nitrogen harvest index (NHI) | = | $(GNY / BNY) \times 100$ | % |
| e. | Nitrogen uptake efficiency (NUpE) | = | BNY / NF | $gg^{-1}N$ |
| f. | Nitrogen utilization efficiency (NUtE) | = | GY / BNY | $gg^{-1}N$ |
| g. | Nitrogen use efficiency (NUE) | = | $NUpE \times NUtE$ | $gg^{-1}N$ |

3.9 Assessing effect of NH_4^+ -N and NO_3^- -N treatment on root growth under soil-filled glass rhizotrons

To assess the degree of variation for root traits under different forms of Nitrogen, a set of selected lines based on phenotypic performance were grown in thin rhizotrons with glass sides that are filled with soil (Fig. 3.4). Root characteristics were measured after 45 days. Plant roots were stored in a 25% ethanol until the scanning procedure. The scanning was performed with a custom flatbed scanner using Winrhizo software. Once the fragment was positioned, its lateral roots were carefully untangled (with a painting brush if needed). The scan was done with a 600 dpi resolution. The same procedure was repeated for every fragment of the root system. The final outputs of the scanning were therefore saved as an image and Microsoft excel data files for different root parameters. Detailed procedure is outlined below.

3.9.1 Materials used

- Plates of 4 mm thick, clear glass cut to 450 × 300 mm.
- Soil sieved using a coarse sieve (approximately 5 mm mesh) to remove stones and large clumps.
- Duct tape, two straight 15 mm thick and 400 mm long wood, 15 mm thick plastic ring and chemicals for nutrient solution.

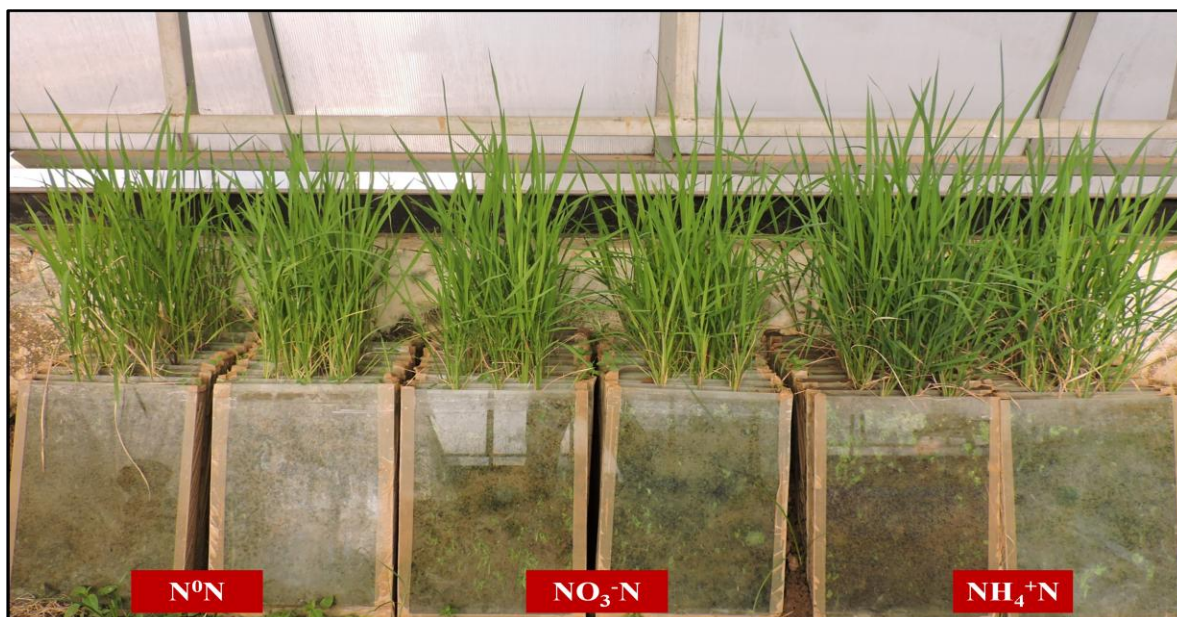


Fig. 3.4 A set of selected lines grown in thin glass rhizotrons

3.9.2 Procedure

- Two clean glass sheets were taken and then one was placed on a work surface with two of the four edges slightly overhanging.
- Two thick woods of 15mm lengths were placed on top of the first sheet, a 15 mm thick plastic ring was placed at the top and the bottom of the glass as spacers and then the second sheet of glass was placed over the top.
- Brown duct tapes were used to join the two sheets of glass together at the overhanging edges. The sheets were turned so that the remaining long edge was overhanging, and that was then sealed with duct tape. Three of the four sides were therefore completely sealed with duct tape.
- The empty rhizotrons was set vertical, a single strip of duct tape was wound right around the rhizotrons at the top and bottom, and the two lengths of wood were removed. The two plastic ring prevented glass from sticking together and empty rhizotrons was stacked.
- One at the top ring was removed at the time of soil-filling process. The plastic ring at the bottom remained in the rhizotron. The empty rhizotrons was

balanced straight upon a soft support *i.e.* expanded polystyrene sheet and sieved soil was then encouraged into the rhizotrons. When the rhizotrons was nearly full, the upper ring was removed and gently tapped on the support. This caused the soil level drop by 10-15 cm due to packing of the soil. The rhizotrons was refilled, gently tapped once more and finally refilled to 5 mm at the top.

- During watering, there is a tendency for the soil to move down. This is minimal if the rhizotron is well packed with soil (not loose) and if water is applied slowly. Practice packing and watering before deciding on the amount of soil to use.
- A small drainage hole was made at each side at the bottom using a sharpened pencil.
- Rhizotrons were placed in stacks of eight and was leaned at an angle of 15° to encourage roots to grow on the lower face. The exposed face of the first stack was backed with an insulation sheet to reduce heat exchange and prevent light penetration.
- Three seeds were sown in each rhizotron and thinned to one when they have emerged completely.
- Watering is typically done two times a week with 250 ml of nutrient solution for the first three weeks, moving to larger volumes of nutrient and water as plant grows. Weeding was also done on regular intervals. Proper application of nutrient solution was followed up to 45 days.
- Rhizotrons was photographed with a high-resolution (12 mega pixel) digital camera on the final day of experiment.
- At the end of the experiment, plants were removed to assess various parameters under study.
- Roots were subjected to washing in an area under continuous supply of water to remove all loose soil.

3.9. 3 Root washing

3.9.3.1 Materials required for root washing

Large plastic containers, 50 ml Tarson tube, metal forceps, small plastic container, markers for labelling and 25% ethanol.

3.9.3.2 Procedure for root washing

Tarson tubes for root samples were prepared first, with the exact sample name. For root scanning the roots were washed with tap water two times. Roots were preserved in ethanol solution (25%) in 50 ml Tarson tubes for root scanning. The procedure was conducted cautiously to prevent supplementary root damage and losses. Debris and dead roots were removed from vital roots.

3.9.4 Root scanning

Root studies were followed according the root scanning protocol given by International Rice Research Institute (IRRI), Philippines. After 45 days, samples were collected for root scanning. Protocol used for root scanning (www.irri.org) under three steps (a) Root studies under soil filled glass rhizotrons (b) root washing and (c) root scanning.

3.9.4.1 Materials used for root scanning

Plastic forceps, Water, Plexiglas trays (Acrylic trays) for WinRhizoReg 2009 scanner (clean with no scratches), computer, Win RhizoReg 2009 USB key.

3.9.4.2 Procedure for root scanning

The stored roots of each line were used for root scanning. The roots of three plants from each line were used for root scanning which given the detailed information about all root parameters including root length, root volume, root diameter, root tips, number of forks etc. The root scanning was done by using root scanner machine Epson Perfection V700/ V750, 3.81 Version, WinRhizoReg 2009, the data was recorded automatically in the computer for different root parameters including root length, average root diameter, root volume, number of tips, forks, surface area etc.

a) Preparing roots for scanning

The acrylic trays were first washed with water and dried completely, the tray was filled with clear clean water and the roots were placed in tray. Roots were then floated in water in acrylic trays on the scanner, this allows the roots to be arranged so as to reduce overlap and crossing of roots. Plastic forceps was used tool for arranging the roots in specific manner, this is delicate work; good lighting and steady hands are helpful.

b) Scanning roots

For best results, WinRhizoReg 2009 with an approved scanner used for root scanning, which allow the roots to be light from above and below while the roots were being scanned. This is an important feature (called "Dual Scan" in Regent's documentation), which reduces shadows on the root image. The Regent Positioning System allows the trays to be consistently placed, thus obviating the need to preview each scan. Optimum scanning resolution depends on the type of samples. Generally roots scanned at 600 dpi in 10x15 cm trays. Root length analysis was carried out with grayscale images.

c) The right Threshold value

Analysis results can be sensitive to the threshold parameters used. WinRhizo can automatically set these; one you may manually tweak them from time to time. The color traces on the root indicate where roots have been detected.

d) Analyzing scanned images

The image was analyzed by selecting the region of interest, and it is analyzed. When scanned images are analyzed, the software uses thresholding to determine what is root and what not root is. A few second later, the analysis was complete and roots found by WinRHIZO were identified by colored line in image. The colors used for drawing them are coded according to root diameter. Portions of the image can be excluded from analysis if necessary, and there are basic editing tools if minor image editing is required.

e) Save the measurement data

The last step of the analysis was data saving WinRHIZO knows when data was easily recordable by many programs including spreadsheet style like Excel. Image and their analysis were also saving to file for later validation, reanalysis, or for visualization in other software programs.

3.9.5 Observations recorded under soil filled Glass rhizotron

The observations for physiological traits contributing for root traits were recorded at plant specific stage from each rhizotron plate. The plants from each line were taken for recording the observation such as root length, root volume and average diameter.

Table: 3.6 Observations recorded after root scanning using WinRhizo software

S.N.	Trait	Stage
1	Root length (cm)	45 DAS
2	Root volume (WinRhizo)	45 DAS
3	Average diameter (mm)	45 DAS

3.9.5.1 Root length

Root length was measured in centimeters (cm) from base to tip of root using standard scaling method.

3.9.5.2 Root Volume

It is the area occupied by roots which is analyzed by WinRhizo software after scanning of root in root scanner.

3.9.5.3 Root Diameter

Average diameter of all type of roots (primary, secondary, tertiary) present in a single plant; which was analyzed by WinRhizo software after scanning of root in root scanner.

3.10 Molecular studies

A set of selected 38 genotypes and 32 RILs lines along with the parents (Swarna and Basmati-370) were used for molecular studies.

3.10.1: Genomic DNA isolation

DNA was isolated by modified CTAB method of DNA extraction for rice

- The leaf were cut in a 2 ml Eppendorf tube.
- Added 700 µl CTAB Buffer in this. Add bits.
- Grinded the leaf & add some more CTAB (300 µl)
- Keep it in water bath for 20 min @ 65°C.
- Add 700 µl of Chloroform: Isoamylalcohol (24:1).
- Vortex the sample.
- Centrifuge it for 5 min @ 14000 rpm.
- Transferred upper clear layer in new 1.5 ml Eppendorf tube.
- Add 700 µl of Chloroform: Isoamylalcohol (24:1).
- Vortex the sample.
- Centrifuge it for 5 min @ 14000 rpm.
- Transferred upper clear layer in new 1.5 ml eppendorf tube.
- Add 70 µl (1/10th of supernatant) of 3 M Sodium Acetate and 400 µl of chilled isopropanol in this & kept it for incubation at 4°C for 2 hours or - 20°C for overnight.
- Centrifuged @14000 rpm for 20 min and discard the supernatant.
- Then wash the pellet with 70% ethanol (50 µl).
- Centrifuge it for 3 min @14000 rpm.
- Air dry the pellet.
- Add 100 µl of TE Buffer and dissolved

3.10.2 Quantification of DNA

The DNA samples were quantified on Nano Drop Spectrophotometry (NANODROP 2000c). After quantification, the DNA was diluted with nuclease, protease free water at the final concentration of approximately 50 ng/µl. This was further used for PCR analysis.

3.10.3 PCR amplification SSR primers

1 µl of diluted template DNA of each genotype was dispensed at the bottom of 96 well PCR plates (AXYGEN/TARSON). Separately cocktails were prepared in an eppendoff tube as described in Table 3.7. 9 µl of cocktail was added in each tube.

Table: 3.7 PCR mix for one reaction (Volume 10 µl)

Reagent	Stock concentration	Volume (µl)
Sterile and nanopure H ₂ O	-	5.95
PCR buffer with 15 mM MgCl ₂	10 X	1.0
dNTPs (Mix)	1 mM	1.0
Primer (reverse and forward)	5 µM	1.0
<i>Taq</i> polymerase	5 U /µl	0.05
DNA template	40 ng/µl	1.0
Total		10.0

Table: 3.8 Temperature profile used for PCR amplification using microsatellite markers

Temperature (°C)	Duration (min.)	Cycles	Activity
94	4	1	Denaturation
94	0.45	↑	Denaturation
55	0.30	34	Annealing
72	0.45	↓	Extension
72	7	1	Final Extension
4	24 hrs	1	Storage

The mixture was carried out for 34 cycles in 96 well PCR, thermal cycler (Applied Biosystems Life technologies, USA). Temperature profile for PCR is presented in Table 3.8. After the PCR reaction was completed, 3 µl of 6 X loading dye was added to 10 µl PCR amplicons and 6.5 µl (PCR product with dye) was loaded on 5 % PAGE in a vertical electrophoresis system (CBS scientific) along with 50 bp ladder (Genei/Merech Bioscience Pvt. Ltd.). Electrophoresis was done for 1 hour at 160 volts. Gels were stained using EtBr solution then visualized and photographed by using Gel Doc Unit, BIO-RADgeldocXR+.

3.10.4. Detection of parental and varietal polymorphism and Development of genotypic data of population by using SSR primers

In case of 38 germplasm lines, varietal polymorphism was detected by using 22 SSR primers. The primers used for this purpose and their scoring are listed in Appendix-C.

The parental polymorphism of RILs was detected by using eighty two SSR primers (ILS/Sigma Aldrich) were taken. The primer exhibited polymorphism between parents was further used for PCR amplification on all of the 32 RILs of rice. Genotypic data were generated with a set of 17 polymorphic primers. The primers used for this purpose and their scoring are listed in Appendix-D.

3.10.5 Scoring and analysis of data

The banding pattern of population developed by each set of primer was scored separately for both germplasm and RILs. The size of amplified fragments was determined by comparing the migration distance of amplified fragments relative to the molecular weight of known size markers, 50 base pairs (bp) DNA ladder. For germplasm particular base pair position was scored as “1” and absence of band for that particular base pair position was scored as “0” (zero). For analysis NTSYS-pc software was used to construct a UPGMA (unweighted pair group method with arithmetic averages) dendrogram showing the distance-based interrelationship among the genotypes and for RILs banding pattern of population scored separately (Table 3.9).

Table: 3.9 Scoring SSR banding pattern in RILs population

Sr. No.	Code	Type of band
1	1	Swarna
2	0	Basmati-370
3	NA	Not amplified

3.11. Preparation of Buffers and chemicals

3.11.1 Estimation of grain and straw nitrogen

- a. **15% NaOH:** Dissolve 150 g of NaOH in 1000 ml of distilled water.
- b. **40% NaOH:** Dissolve 400 g of NaOH in 1000 ml of distilled water.

- c. **4 % Boric acid:** Dissolve 40 g of boric acid in 800 ml distilled water. Make volume to 1 liter.
- d. **Mixed indicator:** Take 0.066 gm of bromocresol green and 0.033 gm of methyl red, then dissolved in 100 ml of absolute ethanol.
- e. **Boric acid indicator:** Take 800 ml of 4% boric acid solution and add 20 ml of mixed indicator, then make volume upto 1 liter.
- f. **catalyst mixture:** Take K_2SO_4 and $CuSO_4$ in 1:10 ratio and mix it properly.
- g. **0.05 N sulphamic acid:** Dissolve 4.854 of sulphamic acid in 800 ml of distilled water and dilute the solution to 1Liter.

3.11.2. Reagents for PCR

- a. **Primers:** Highly variable microsatellite markers from ILS, USA
- b. **dNTPs: (dATP/dCTP/dGTP/dTTP):** 1 mM stock of dNTP (GeNei) was used.
- c. **PCR buffer (10 X):** From Genei Mereck Bioscience Pvt Ltd along with $MgCl_2$.
- d. **Taq polymerase:** 1 unit/ μ l, 1000 U *taq* (GeNei) was used for PCR.

3.11.3. Stock solutions

a. Preparation of DNA extraction buffer

- 100 mM Tris HCl- 2.42 g
- 1.4 M NaCl- 16.36
- 20 mM EDTA- 1.49 g
- CTAB- 6 g

Volumes make upto 200 ml by Double Distilled Water and Autoclave for 20 min.

b. TE buffer

- 1 M Tris-HCl (pH-8) 1 ml
- 0.5 M EDTA 0.2 ml

Final volume was adjusted to 100 ml and autoclaved

c. EDTA (0.5M, pH-8)

186.12 g of EDTA was dissolved in 700 ml of distilled water. NaOH pallets were added for proper dissolving of EDTA. The pH was set to 8 using NaOH/HCl.

Final volume was adjusted to 1000 ml with distilled water and sterilized by autoclaving.

d. 4 M NaCl

35.04 g of NaCl was dissolved in 100 ml of distilled water. Final volume was adjusted to 150 ml and sterilized by autoclaving.

e. 1 M Tris HCl (pH 8.0 at 25°C)

31.52 g of Tris Cl/Trizma base was dissolved in 100 ml of distilled water. The pH was set to 8.0 using concentrated HCl. The final volume was adjusted to 200 ml with distilled water and sterilized by autoclaving.

f. Absolute alcohol (pre chilled)

g. 70 % Ethanol

70 ml of absolute ethanol was taken and volume makeup 100 ml with distilled water.

3.11.4. Solutions for electrophoresis

a. 10 X TBE buffer

- Tris base 104 g
- Boric Acid 55 g
- EDTA (0.5 M) 40 ml
- Distilled water 500 ml

Final volume was adjusted to 1 litre with distilled water.

b. Tank buffer (1 X TBE)

100 ml of 10 X TBE + 900 ml of distilled water.

c. 5 % Acrylamide gel solution (1000 ml)

- Acrylamide 47.5 g
- Bis-Acrylamide 2.5 g
- 10 X TBE 100 ml

Final volume was adjusted to 1 liter with distilled water.

Acrylamide and bis-acrylamide were weighed and dissolved one by one in 500 ml distilled water then added to 100 ml of 10 X TBE and the volume was made upto

1000 ml by adding autoclaved double distilled water. The solution was sterilized by passing through 0.22 micron and stored in amber colour bottle at 4°C.

d. 10 % Ammonium persulphate (APS)

Ammonium persulphate 1.0 g

Distilled water 10 ml

e. Ethidium bromide

Ethidium bromide powder 10 mg

Water 1 ml

f. Gel staining solution

Ethidium bromide 10 µl

Distilled water 200 ml

g. 6 X loading dye

Bromophenol blue 0.25 g

Glycerol 40 ml

Final volume was adjusted to 100 ml with distilled water.

h. 50 bp DNA ladder (GeNei)

Step up 50 bp ladder (500 µg/ml) 0.1 ml

Gel loading buffer (6 X) 0.2 ml

Water (Nuclease free) 0.4 ml

3.12 Statistical analysis

The data recorded on all the traits related to yield and yield contributing characters under all the seasons were tabulated and statistically analyzed. F-test was used to determine treatment significance.

3.12.1 Analysis of variance

The mean data of each replication was used for analysis of variance using augmented design for wet season 2015. The augmented experimental design introduced (Federer 1956) was used for the experiment. The analysis was performed using IASRI online software and factorial design (three-way ANOVA) for wet season

2016, due to presence of multiple variables in experiments. Skeleton of ANOVA for augmented and factorial design is depicted in Table 3.10 and Table 3.11, respectively.

3.12.2 Parameters of variation

3.12.2.1 Mean

Mean is the average value of observation of genotypes of a series. It represents the standard average value over fluctuation in the environment. Mean was calculated by the following formula:

$$\bar{X} = \Sigma X_i / n$$

Where,

ΣX_i = Summation of all the observations

n = Total number of observations

3.12.2.2 Range

Range is the difference between the highest and the lowest value of a series of observations and thus, provides the information about the extent of variability present in the genotypes.

$$\text{Range} = \text{Highest value} - \text{Lowest value}$$

Table: 3.10 Skeleton of ANOVA table for augmented design

Source	Degree of freedom	Sum of Square	Mean square	F Statistic
Block	b-1	BSS	$MSB = BSS / (b-1)$	MSB / MSE
All Genotype	(g+c)-1	GCSS	$MSGC = GCSS / (g+c)-1$	$MSGC / MSE$
Test Genotype	g-1	GSS	$MSG = GSS / (g-1)$	MSG / MSE
Checks	c-1	CSS	$MSC = CSS / (c-1)$	MSC / MSE
Test vs Checks	1	GvsCSS	$MSG_{vsC} = G_{vsC} / 1$	MSG_{vsC} / MSE
Error	(c-1)(b-1)	ESS	$MSE = ESS / (c-1)(b-1)$	
Total	n-1	TSS		

Table: 3.11 Skeleton of ANOVA table for factorial design

Source of variation	Sum of Squares	Degrees of freedom	mean squares	F statistic
Factor A	SSA	a-1	MSA=SSA/(a-1)	MSA/MSE
Factor B	SSB	b-1	MSB=SSB/(b-1)	MSB/MSE
AB (Interaction)	SSAB	(a-1)(b-1)	MSAB=SSAB/[(a-1)(b-1)]	MSAB/MSE
Error	SSE	N-ab	MSE=SSE/(N-ab)	
Total	SST	N-1		

3.12.2.3 Standard deviation (SD)

Standard deviation is the root of sum of squares of deviation divided by their number, calculated by the formula:

$$\text{Standard deviation} = \sqrt{\Sigma d^2 / n}$$

Where,

Σd^2 = Sum of squares of deviations

n = Total number of observations

3.12.2.4 Standard error of mean is calculated as follows

$$SE_m = \sqrt{\frac{MSe}{r}}$$

The standard error of the difference between any two treatments is expressed by the following formula:

$$SE_d = \sqrt{\frac{2MSe}{r}}$$

Where, MS_e = error mean square

r = number of replications.

The significance of difference among the treatments means was tested by F-test at 5 and 1% level of significance. Whenever the F value was found to be significant, critical difference was calculated to test the significance of difference between any two treatment means as follows:

C.D. (at 5%) = $SE_d \times t\text{-value (5\%)} \text{ at error d.f.}$

3.12.2.5 Coefficient of variation (%)

$$CV = \left(\frac{\sqrt{MSe}}{\bar{X}} \right) \times 100$$

Where, $\bar{X}$ general mean of character

3.12.3 Estimation of Variability

Different coefficients of variances were computed following Burton (1952).

a) Phenotypic coefficient of variation (PCV %)

$$PCV (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

b) Genotypic coefficient of variation (GCV %)

$$GCV (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

3.12.4 Heritability (broad sense)

It is the ratio of genotypic variance to the phenotypic variance (total variance). Heritability for the present study was calculated in a broad sense by adopting the formula as suggested by Hanson *et al.* (1956):

$$h^2(bs) \% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 (bs) = heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The estimates of heritability broad sense were classified as low, moderate and high according to Robinson (1966):

< 50 %	–	Low
50-70 %	–	Moderate
> 70 %	–	High

3.12.5. Estimation of Genetic Advance as percentage of mean

Improvement in the mean genotypic value of progeny of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection.

$$\text{Genetic advance} = h^2_{(bs)} \times \sigma_p \times K$$

$h^2_{(bs)}$ = heritability in broad sense

σ_p = phenotypic standard deviation

K = selection differential at 5% selection intensity

The value of K (at 5% selection intensity) = 2.06 (Allard, 1960)

Genetic advance expressed as per cent of population mean was calculated as follows:

$$\text{Genetic advance as \% of mean} = \frac{\text{Genetic Advance}}{\text{General population mean}} \times 100$$

3.12.6 Character association

3.12.6.1 Correlation coefficient

Correlation coefficients were computed to determine the association among the characters studied. The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance. Correlation coefficient (r) was calculated for grain yield and yield contributing characters by using the standard procedure given by Searle (1961).

Test of significance for correlation coefficient

For testing the significance of r , the t -value was calculated as follows

$$t = \frac{r}{\sqrt{1-r^2}} \sqrt{n-2}$$

Where r is the estimate obtained from n pairs and the ratio is distributed in sampling as t with $(n-2)$ degrees of freedom. The significance for correlation coefficient was tested by comparing observed value of correlation coefficient with tabulated values for $n-2$ degree of freedom. If the observed value is more than the table value, the correlation coefficient is considered to be significant.

3.12.6.2 Path coefficient analysis

The phenotypic and genotypic correlation coefficient were further partitioned into direct and indirect effect with the help of path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The path coefficient was estimated by solving following sets of simultaneous equations indicating the basic relationship between correlation and path coefficients.

$$r_{iy} = P_{iy} + r_{i1}P_{1y} + r_{i2}P_{2y} + \dots + r_{i(i-1)}P_{iy}$$

$$i = 1, 2, 3, \dots, n$$

Where,

i is the no. of independent characters (causes); r_{1y} to r_{iy} denotes coefficient of correlation between independent variables (1..... i) with dependent character y ; r_{i1} to $r_{i(i-1)}$ denotes coefficient of correlation among all possible combination of caused factors (independent variables); P_{1y} to P_{iy} denotes the direct effects of independent variables (1..... i) on the dependent variable y .

3.12.7 Cluster analysis

Cluster analysis is a multivariate method which aims to classify a sample of subjects (or objects) on the basis of a set of measured variables into a number of different groups such that similar subjects are placed in the same group. Cluster analysis has no mechanism for differentiating between relevant and irrelevant variables. Therefore, the choice of variables included in a cluster analysis must be

underpinned by conceptual considerations. This is very important because the clusters formed can be very dependent on the variables included.

In the present study, Euclidian distance between genotypes was calculated from the standardized data matrix by Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method and clustering was done by Agglomerative Hierarchical method using XLSTAT 2014 software.

3.12.8 Stability analysis

Analyzed the data of two years over two environmental locations by using stability model proposed by Eberhart and Russell (1966). The model involves the estimation of mean, regression coefficient and deviation from regression, which are defined by a mathematical formula.

$$Y_{ij} = \mu_i + \beta_i I_j + S_{ij}$$

Where,

Y_{ij} = Mean of the i^{th} genotype at the j^{th} environment

μ_i = Mean of i^{th} genotype over all environments

β_i = Regression coefficient that measures the response of i^{th} genotype to varying environments

I_j = Environmental index obtained by subtracting the grand mean from the mean of all genotypes at the j^{th} environment

S_{ij} = Deviation from regression of the i^{th} genotype at the j^{th} environment

3.13 QTL analysis

Single Marker Analysis was performed with the help of QTL Cartographer 2.5. Graphical genotyping of molecular data was done using GGT 2.0 (Van Berloo, 1999).

CHAPTER - IV

RESULTS AND DISCUSSION

In the present investigation entitled “**Genetical studies on NO_3^- use efficiency under aerobic and anaerobic conditions in rice (*Oryza sativa* L.)**” efforts were made to examine the genetic basis as well as the physiological mechanisms involved in nitrogen uptake and utilization along with grain yield in rice. The numerous data obtained from nitrogen analysis from grain and straw involved in the pathway are integrated into explanatory models to study whole plant/genotype behaviour. The results of the present study are put through statistical analysis to make necessary inferences and are further validated with experimental findings by establishing a cause and effect relationship on the basis of available data which are presented in this chapter.

A set of 116 rice germplasm accessions and seven checks Indira Sona, Indira Aerobic 1, Swarna, Basmati-370, IR-64 (Drought), Samleshwari and Danteshawari were used. The augmented experimental design introduced by Federer (1956) was used for the experiment. An augmented experimental design (AED) is usually useful for testing a large number of genotypes in early generations when valid statistical analyses are needed particularly when seed supplies are too limited to permit replication.

The test entries along with checks were sown by direct seeded with a spacing of 20 cm row to row with two rows for each genotype of 2 meter row length. The field experiment was carried out in wet season 2015 under two different forms of N i.e. N in the form of calcium nitrate (NO_3^-) and N in the forms of ammonium chloride (NH_4^+) along with zero nitrogen (N^0) for both aerobic and anaerobic condition. Data were collected for grain yield and yield contributing traits at the appropriate growth stage of rice plant following the descriptor for Rice *Oryza sativa* L. SES (IRRI, 2002). From each genotype, five random plants are selected for data collection. 85 genotypes,

out 116 along with seven checks and their plot means were analyzed using standard statistical analysis suggested by Federer (1956). The remaining genotypes did not survived as the reproductive and ripening phase were vulnerable and crucial for moisture stress, which resulted in permanent damage to growth and yield. Row and Venkateswarlu (1983) and Wopereis *et al.* (1996) also reported that water stress during flower induction and inflorescence development lead to delay in flowering (anthesis) and reduces grain yield.

In another set 179 RILs between Swarna X Basmati-370 was sown in aerobic condition under different nitrogen regimes. The simple selection criteria were applied for promoting the lines. On the basis of yield performance 32 lines along with parents were selected for further single marker analysis.

4.1 Analysis of Variance for augmented design (wet season 2015)

The analysis of variance revealed significant differences between test genotypes and checks for most of the characters under varied nitrogen regimes and environments (Table 4.1). The results indicated high variances for most of the characters and genotypic response of different nitrogen regimes which may favour the selection and its further utilization in breeding programmes in the mere future.

4.1.1 Mean performance of germplasm

Mean phenotypic performance and range with respective germplasm accession for 11 characters under different nitrogen regimes for both aerobic and anaerobic condition during wet season 2015 are presented in Table 4.2. Higher values were observed for all the studied traits at the NH_4^+ treatment followed by NO_3^- and N^0 treatment across both environments.

In aerobic condition days to 50% flowering under N^0 condition ranged from 71 to 110 days with a mean of 92 days, under NO_3^- condition it ranged from 67 to 110 days with mean of 92 days and under NH_4^+ condition it varied from 69 to 111 days with mean of 93. In anaerobic condition under N^0 it ranged from 63 to 107 days with mean of 90 days, under NO_3^- condition it ranged from 65 to 107 days with the mean of

90 days, while under NH_4^+ condition it was ranged from 62 to 110 days with mean of 89 days.

Plant height at seedling ranged from 17.31 to 34.98 cm under N^0 , 21.68 to 35.03 cm under NO_3^- and 21.78 to 44.68 cm under NH_4^+ condition for aerobic condition while overall mean of plant height at seedling was 25.47, 27.41 and 28.84 cm under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition it ranged from 41.37 to 80.67 cm with phenotypic mean of 55.69 cm under N^0 , it ranged 43.24 to 79.10 cm with mean of 56.46 cm under NO_3^- and under NH_4^+ condition it varied from 49.18 to 92.27 cm with overall phenotypic mean of 64.80 cm.

Under aerobic condition, in N^0 treatment, value of chlorophyll content at flowering ranged from 26.44 to 43.73 with a mean phenotypic value of 33.98. In NO_3^- range of variation for chlorophyll content was 30.06 to 44.56 with mean phenotypic value of 37.63. While in NH_4^+ treatment, it ranged from 30.98 to 46.41 showing average value of 39.40. In anaerobic condition chlorophyll content at flowering ranged from 22.54 to 40.53 with mean value of 33.01 under N^0 . Whereas in NO_3^- and NH_4^+ ranged from 24.01 to 44.64 with average value of 36.14 and from 22.87 to 37.77 with mean value of 37.77 respectively.

Under aerobic condition plant height at maturity varied from 50.83 to 130.81 cm, 51.50 to 129.88 cm and 52.75 to 153.81 cm with mean phenotypic value of 84.10, 90.58 and 99.26 cm under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition under N^0 it varied from 60.31 to 144.10 cm with mean of 106.56 cm, under NO_3^- was ranged from 74.54 to 160.70 cm with mean of 112.80 cm and under NH_4^+ it ranged from 80.92 to 178.34 cm with phenotypic mean of 113.90 cm.

Number of effective tillers per plant ranged from 3.69 to 8.06, 3.81 to 8.32 and 4.23 to 8.03 under N^0 , NO_3^- and NH_4^+ respectively and means phenotypic value was 5.55 under N^0 , 5.67 under NO_3^- and under NH_4^+ 6.56.

Panicle length ranged from 17.26 to 25.18 cm under N^0 , 17.45 to 26.49 cm under NO_3^- and 19.07 to 27.80 cm under NH_4^+ condition for aerobic condition with overall mean of plant 21.48, 22.52 and 23.21 cm under N^0 , NO_3^- and NH_4^+ respectively.

Table: 4.1 ANOVA for yield and yield contributing traits under N⁰, NO₃⁻ and NH₄⁺ form of nitrogen and variable environments during wet season-2015

		Aerobic						Anaerobic					
Traits	N	Block	All genotypes	Test genotypes	Checks	Test Vs Checks	Error	Block	All genotypes	Test genotypes	Checks	Test Vs Checks	Error
		DF=4	DF=91	DF=84	DF=6	DF=1	DF=24	DF=4	DF=91	DF=84	DF=6	DF=1	DF=24
DF	N ⁰	5.95	59.00*	43.68*	296.22*	2.39	2.99	11.18*	49.11*	35.13*	249.84*	22.13*	2.25
	NO ₃ ⁻	8.32**	68.83*	46.45*	392.22*	5.39	2.81	0.529	56.40*	39.58*	295.04*	42.52*	1.84
	NH ₄ ⁺	8.71	69.75*	48.06*	362.82*	99.31*	4.19	8.81	65.06*	44.34*	344.78*	138.04*	1.61
PHSD	N ⁰	10.21	13.84*	11.32**	24.09*	144.09*	5.36	24.97**	62.48*	49.39*	158.61*	547.21*	7.42
	NO ₃ ⁻	5.56	9.70**	7.56	34.99*	34.55**	5.05	11.47**	71.63*	57.20*	206.09*	417.44*	4.09
	NH ₄ ⁺	7.65	16.44*	14.75*	40.15*	10.91	4.17	273.88*	94.31*	73.62*	201.88*	1193.93*	12.74
CCSD	N ⁰	32.99*	8.64**	7.46**	22.66*	15.25	4.14	3.36	6.12	5.27	13.25	28.66**	5.69
	NO ₃ ⁻	21.66*	7.21**	6.30**	12.49**	34.11*	3.45	9.44	11.02	10.48	9.37	50.20**	7.47
	NH ₄ ⁺	13.46*	7.65*	7.17**	9.85**	37.70*	3.11	27.26**	10.87	8.74	22.51**	117.33*	7.50
CCFW	N ⁰	20.93**	13.14*	13.71*	7.40	0.12	5.36	1.38	9.24**	9.08**	12.16**	3.55	4.47
	NO ₃ ⁻	4.90	7.67**	8.12*	2.65	0.62	3.41	3.87	17.53*	17.60*	17.54**	11.56	6.67
	NH ₄ ⁺	4.03	6.64	6.80	4.12	5.53	5.28	7.28	21.74**	20.21**	21.13	162.04*	10.11
PHMT	N ⁰	116.22*	232.07*	208.63*	554.76*	143.37*	14.84	117.86*	860.49*	817.26*	1527.52*	277.45*	17.1
	NO ₃ ⁻	12.32	255.05*	228.39*	666.06*	9.99	27.98	31.9	585.42*	502.03*	1646.05*	1056.80*	15.02
	NH ₄ ⁺	63.79	290.87*	257.28*	797.54*	12.15	35.22	195.49*	413.42*	322.67*	1579.26*	858.81*	18.31
ET	N ⁰	-	-	-	-	-	-	0.53	0.61**	0.61**	0.61	0.2	0.27
	NO ₃ ⁻	-	-	-	-	-	-	0.64	0.79	0.73	0.89	4.61*	0.53
	NH ₄ ⁺	-	-	-	-	-	-	1.27**	0.52	0.49	0.93**	0.30	0.36

Table: 4.1 continued...

PL	N ⁰	2.33	2.82	2.38	8.58*	6.53	1.93	4.24	3.04	1.95	15.99*	12.58**	1.75
	NO ₃ ⁻	1.39	3.80*	3.02*	11.67*	22.34*	1.20	3.16*	4.12*	2.63*	19.93*	28.22*	0.58
	NH ₄ ⁺	0.60	4.22*	2.97**	16.50*	39.34*	1.60	2.27	4.52**	3.31	20.98*	6.94	2.17
SPP	N ⁰	407.40	1169.76*	1170.39*	1051.81*	1613.35**	230.29	1617.22*	1439.53*	1002.00*	7032.47*	3653.93*	173.39
	NO ₃ ⁻	75.58	768.84*	736.50*	658.34*	4322.37*	168.71	1550.97*	1810.21*	1210.59	10233.74	2094.09*	264.62
	NH ₄ ⁺	459.79	945.92*	880.72*	1200.66*	5030.66*	201.44	1303.86**	2025.43*	1243.75*	11448.34*	11189.15*	312.16
FGP	N ⁰	197.85**	635.08*	618.97*	279.28*	3553.48*	59.60	754.91*	1170.39*	857.99*	4658.73*	4989.20*	85.97
	NO ₃ ⁻	53.96	653.42*	609.36*	324.09*	6304.15*	73.96	749.40*	1324.15*	964.76*	6569.79*	148.82	148.44
	NH ₄ ⁺	264.69**	852.27*	797.00*	229.80**	9342.06*	69.44	892.72**	1445.91*	925.21*	7874.77*	6667.58*	213.30
SF	N ⁰	6.89	102.50*	98.27*	62.19	591.91*	38.77	87.13	53.32	44.1	162.62*	111.53	41.54
	NO ₃ ⁻	21.16	83.59**	80.44**	16.64	701.99*	44.19	22.63	48.73	46.26	51.78	210.31**	48.10
	NH ₄ ⁺	4.94	140.48*	124.91*	91.54	1705.17*	36.89	39.31	57.92	59.03	48.83	20.35	34.64
TW	N ⁰	0.006	0.065*	0.052*	0.240*	0.085*	0.004	0.059*	0.041*	0.115*	0.444*	0.648*	0.009
	NO ₃ ⁻	0.040	0.088*	0.070*	0.290*	0.000	0.270	0.071*	0.145*	0.130*	0.359*	0.122*	0.013
	NH ₄ ⁺	0.064**	0.072*	0.063*	0.210*	0.000	0.020	0.063*	0.102*	0.081*	0.392*	0.132*	0.014
GY	N ⁰	2555.84	5367.40*	4425.55*	17060.07*	9250.23**	1267.64	2914.81	12202.08*	8849.91*	59984.09*	6690.99	2308.11
	NO ₃ ⁻	748.92	7762.10*	5568.74**	29027.64*	58576.23*	2548.01	7461.37	11724.95*	8958.09*	52141.50*	1704.4	3775.24
	NH ₄ ⁺	2905.91	9621.43*	7413.84*	29857.85*	72322.58*	2128.33*	9604.73	19687.56*	13742.06**	85462.19*	104492.46*	6937.16

* and ** significance at .05 and .01 levels respectively, N- Forms of nitrogen. **DF**-Days to 50% flowering; **PHSD**-Plant height at seedling (cm); **CCSD** and **CCFW**-SPAD reading at seedling and flowering stage, respectively; **PHMT**-Plant height at maturity (cm); **ET**-Effective tillers per plant; **PL**-Panicle length (cm); **SPP**-Number of spikelet per panicle; **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²).

Table: 4.2 Mean phenotypic performance, range and their respective germplasm accession name for yield and yield contributing traits under different N regimes and environments during wet season-2015

Traits	N	Aerobic				Anaerobic			
		Range and Genotype				Range and Genotype			
		Mean	Min	Genotype	Max	Genotype	Min	Genotype	Max
DF	N ⁰	91.55	70.97	Neha	109.83	Sampada	89.95	63.09	106.51
	NO ₃ ⁻	91.85	68.94	Neha	109.60	Swarna	89.53	64.89	106.89
	NH ₄ ⁺	92.88	69.43	Neha	111.29	R -RHZ-II-22	88.89	61.83	109.54
PHSD	N ⁰	25.47	17.31	R 1744-4901-1-1-510-1	34.98	Barangi	55.69	41.37	80.67
	NO ₃ ⁻	27.41	21.68	R 1262-1667-1-1	35.03	Barangi	56.46	43.24	79.10
	NH ₄ ⁺	28.84	21.78	R 1860-783-1-424-1	44.68	Anjan II	64.80	49.18	92.27
CCSD	N ⁰	32.55	25.04	Mauhakuchi	39.99	R 1033-968-2-1	33.57	28.56	39.29
	NO ₃ ⁻	35.91	29.67	CGR-547 (Bargi)	41.91	R-RHZ-2	34.70	27.54	44.35
	NH ₄ ⁺	38.37	27.87	Mahamaya	47.07	Indira Barani Dhan-1	34.94	27.39	42.50
CCFW	N ⁰	33.98	26.44	Bhajna	43.73	R 2212-RF-75	33.01	22.54	40.53
	NO ₃ ⁻	37.63	30.06	Bhajna	44.56	R 1670-3975-1-485-1	36.14	24.01	44.64
	NH ₄ ⁺	39.40	30.98	Kendumudi- 1	46.41	R 1695-270-2-133-1	37.77	22.87	49.21
PHMT	N ⁰	84.10	50.83	Neha	130.81	Jogi Bhog	106.56	60.31	146.30
	NO ₃ ⁻	90.58	51.50	Neha	129.88	Jogi Bhog	112.80	74.54	160.70
	NH ₄ ⁺	99.26	52.75	Neha	153.81	Anjan II	113.90	80.92	178.34
ET	N ⁰	-	-	-	-	-	5.55	3.69	8.06
	NO ₃ ⁻	-	-	-	-	-	5.67	3.81	8.32
	NH ₄ ⁺	-	-	-	-	-	6.56	4.23	8.03

N-Forms of nitrogen. **DF**-Days to 50% flowering; **PHSD**-Plant height at seedling (cm); **CCSD and CCFW**-SPAD reading at seedling and flowering stage, respectively; **PHMT**-Plant height at maturity (cm); **ET**-Effective tillers per plant.

Table: 4.2 Continued...

Traits	N	Aerobic				Anaerobic			
		Range and Genotype				Range and Genotype			
		Mean	Min	Genotype	Max	Genotype	Min	Genotype	Max
PL	N ⁰	21.48	17.26	Neha	25.18	BRR-0006	23.32	16.36	26.16
	NO ₃ ⁻	22.52	17.45	Neha	26.49	Anjan (CGR-1814)	24.84	17.41	29.37
	NH ₄ ⁺	23.21	19.07	Tewan Dhan	27.80	IR 84887-B-15	24.13	17.11	29.44
SPP	N ⁰	119.02	25.89	Neha	199.09	Indira Barani Dhan 1	150.93	59.37	254.69
	NO ₃ ⁻	121.70	60.61	IGKVR 1244	172.18	RCPR 8	154.98	44.70	232.39
	NH ₄ ⁺	124.82	49.46	Neha	193.23	Indira Barani Dhan 1	152.67	58.57	278.63
FGP	N ⁰	89.64	14.63	Neha	140.86	R 1570-2649-1-1546-1	123.45	44.30	206.53
	NO ₃ ⁻	94.39	43.69	Tewan Dhan	140.49	Indira Barani Dhan 1	131.65	36.43	206.86
	NH ₄ ⁺	94.75	37.62	CB 09 512	150.82	R 1860-783-1-424-1	130.10	36.37	200.52
SF	N ⁰	75.88	44.86	Anjan (CGR-1814)	90.23	R 1700-309-1-171-1	81.55	58.94	96.26
	NO ₃ ⁻	77.20	44.03	Rajniti (A)	93.47	R 1700-309-1-171-1	85.16	62.84	99.32
	NH ₄ ⁺	75.19	41.99	Chhota Dhan	92.53	RCPR 8	85.50	55.06	99.89
TW	N ⁰	1.83	1.30	Anjan 1	2.37	R 1695-270-2-133-1	2.55	1.82	3.44
	NO ₃ ⁻	2.13	1.20	BRR-0006	2.69	R 1917-951-1-541-1	2.47	1.57	3.55
	NH ₄ ⁺	2.14	1.26	R 1240-913-2-1013-1	2.69	R 1747-4941-1-515-1	2.48	1.73	3.17
GY	N ⁰	159.81	21.11	R 1641-914-1-400-1	356.46	Digamber Dhan	398.80	135.19	599.36
	NO ₃ ⁻	190.80	41.04	Bhajna	361.93	R -RHZ-2	448.39	144.07	734.31
	NH ₄ ⁺	200.65	25.71	R 741-1-55-2-1-R-1	391.25	Dadhmaini Dhan	469.68	111.17	658.55

N-Forms of nitrogen. **PL**-Panicle length (cm); **SPP**-Number of spikelet per panicle; **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²).

In anaerobic condition panicle length ranged from 16.36 to 26.16 cm with phenotypic mean of 23.32 cm under N^0 , it ranged from 17.41 to 29.37 with mean of 24.84 cm under NO_3^- and under NH_4^+ condition it varied from 17.11 to 29.44 cm with overall phenotypic mean of 24.13 cm.

Under aerobic condition for N^0 , number of spikelets per panicle ranged from 25.89 to 199.09 with overall mean of 119.02 while under NO_3^- condition it varied from 60.61 to 172.18 with mean of 121.70 and under NH_4^+ condition it varied from 49.46 to 193.23 with mean of 124.82. Whereas in anaerobic under N^0 condition it ranged from 59.37 to 254.69 with average of 150.93, under NO_3^- condition it ranged from 44.70 to 232.39 with mean of 154.98 and under NH_4^+ condition it ranged from 58.57 to 278.63 with mean of 152.67.

In aerobic condition numbers of filled grains per panicle varied from 14.63 to 140.86 with mean of 89.64 under N^0 condition while under NO_3^- and NH_4^+ conditions it ranged from 43.69 to 140.49 and 37.62 to 150.82 with overall mean of 94.39 and 94.75 respectively. Whereas in aerobic condition, mean of numbers of filled grains per panicle was 123.45, 131.65 and 130.10 under N^0 , NO_3^- and NH_4^+ respectively while it ranged from 44.30 to 206.53 under N^0 , 36.43 to 206.86 under NO_3^- and 36.37 to 200.52 under NH_4^+ .

Spikelet fertility ranged from 44.86 to 90.23 per cent under N^0 , 44.03 to 93.47 per cent under NO_3^- and 41.99 to 92.53 per cent under NH_4^+ for aerobic condition with overall mean of spikelet fertility was 75.88, 77.20 and 75.19 per cent under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition under N^0 spikelet fertility ranged from 58.94 to 96.26 percent with mean of 81.55 per cent, under NO_3^- it ranged 62.84 to 99.32 per cent with mean of 85.16 per cent and under NH_4^+ condition it varied from 55.06 to 99.89 per cent with average of 85.50 per cent.

In aerobic condition test weight under N^0 condition ranged from 1.30 to 2.37 g with a mean of 1.83 g, under NO_3^- condition it ranged from 1.20 to 2.69 g with mean of 2.13 g and under NH_4^+ condition it varied from 1.26 to 2.69 g with mean of 2.14 g. In anaerobic condition under N^0 it ranged from 1.82 to 3.44 g with mean of 2.55 g,

while under NO_3^- condition it ranged from 1.57 to 3.55 g with the mean of 2.47 g and under NH_4^+ condition, it was ranged from 1.73 to 3.17 g with mean of 2.48 g.

In aerobic condition the character grain yield ranged from 21.11 to 356.46 g/m^2 under N^0 , 41.04 to 361.93 g/m^2 under NO_3^- and 25.71 to 391.25 g/m^2 under NH_4^+ condition with overall mean was 159.81, 190.80 and 200.65 g/m^2 under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition under N^0 grain yield ranged from 135.19 to 599.36 g/m^2 with mean of 398.80 g/m^2 , while under NO_3^- it ranged 144.07 to 734.31 g/m^2 with mean of 448.39 g/m^2 and under NH_4^+ condition it varied from 111.17 to 658.55 g/m^2 with average of 469.68 g/m^2 .

4.1.2 Mean performance of RILs

The mean phenotypic performance of RILs and their range along with respective line number for 11 characters recorded during wet season 2015 across differential N regimes under aerobic condition is presented in Table 4.3.

During wet season 2015, under aerobic condition in N^0 treatment, days to 50% flowering ranged from 78 to 103 days with a mean value of 89 days. While it ranged 77 to 107 days with mean phenotypic value of 90 days under NO_3^- and under NH_4^+ it varied from 78 to 106 days with mean value of 91 days. Plant height at seedling was ranged from 24.63 to 42.25 cm, 28.13 to 45.88 cm and 29.13 to 49.80 cm with mean value of 32.64, 36.14 and 37.67 cm under N^0 , NO_3^- and NH_4^+ conditions respectively. Chlorophyll content at seedling ranged from 26.87 to 39.90 with mean of 35.03 under N^0 , whereas it ranged from 31.93 to 48.10 with phenotypic mean of 38.96 under NO_3^- and under NH_4^+ , it ranged from 32.90 to 44.47 with mean of 39.13. While chlorophyll content at flowering ranged from 23.30 to 40.30 under N^0 , 31.50 to 45.90 under NO_3^- and 31.90 to 49.30 under NH_4^+ with mean phenotypic value of 33.17, 37.39 and 39.45 under N^0 , NO_3^- and NH_4^+ conditions respectively.

Under N^0 condition plant height at maturity ranged from 24.20 to 151.70 cm with mean value of 112.44 cm. Under NO_3^- it ranged from 78.10 to 157.60 cm with mean of 122.99 cm and under NH_4^+ it varied from 84.60 to 166.86 cm with phenotypic mean of 127.08 cm.

Table: 4.3 Mean phenotypic performance, range with respective line Number, standard deviation, standard error of RILs population for yield and yield contributing traits under different N regimes for aerobic condition during wet season-2015

Traits	N	Mean	Range and Line No.				SD	SE
			Min	Line No.	Max	Line No.		
DF	N ⁰	89.21	78.00	RIL-174	103.00	RIL-99	5.52	0.58
	NO ₃ ⁻	90.29	77.00	RIL-174	107.00	RIL-6	6.12	0.65
	NH ₄ ⁺	91.30	78.00	RIL-174	106.00	RIL-102	6.55	0.69
PHSD	N ⁰	32.64	24.63	RIL-98	42.25	RIL-39	3.37	0.59
	NO ₃ ⁻	36.14	28.13	RIL-158	45.88	RIL-166	4.03	0.67
	NH ₄ ⁺	37.67	29.13	RIL-170	49.80	RIL-89	4.68	1.69
CCSD	N ⁰	35.03	26.87	RIL-34	39.90	RIL-152	2.46	2.43
	NO ₃ ⁻	38.96	31.93	RIL-178	48.10	RIL-27	2.65	0.43
	NH ₄ ⁺	39.13	32.90	RIL-116	44.47	RIL-14	2.19	2.69
CCFW	N ⁰	33.17	23.30	RIL-70	40.30	RIL-81	3.29	0.58
	NO ₃ ⁻	37.39	31.50	RIL-33	45.90	RIL-131	2.89	0.47
	NH ₄ ⁺	39.45	31.90	RIL-115	49.30	RIL-43	3.02	3.69
PHMT	N ⁰	112.44	24.20	RIL-119	151.70	RIL-75	17.81	1.68
	NO ₃ ⁻	122.99	78.10	RIL-147	157.60	RIL-100	16.26	1.47
	NH ₄ ⁺	127.08	84.60	RIL-147	166.86	RIL-121	15.95	4.69
PL	N ⁰	24.86	18.80	RIL-81	30.60	RIL-82	2.69	0.54
	NO ₃ ⁻	25.52	19.40	RIL-102	32.50	RIL-100	2.65	0.52
	NH ₄ ⁺	26.00	21.10	RIL-102	33.80	RIL-111	2.39	5.69
SPP	N ⁰	122.45	33.00	RIL-129	303.00	RIL-167	36.52	3.30
	NO ₃ ⁻	123.26	46.33	RIL-121	219.33	RIL-56	34.73	3.12
	NH ₄ ⁺	122.01	46.33	RIL-129	197.33	RIL-56	31.43	6.69
FGP	N ⁰	73.24	11.33	RIL-141	203.33	RIL-167	28.44	3.32
	NO ₃ ⁻	72.68	7.00	RIL-141	124.50	RIL-172	27.51	3.23
	NH ₄ ⁺	70.82	13.33	RIL-111	129.67	RIL-166	28.76	7.69
SF	N ⁰	59.74	16.37	RIL-139	90.74	RIL-37	15.25	1.97
	NO ₃ ⁻	58.80	11.67	RIL-141	86.55	RIL-21	16.28	2.12
	NH ₄ ⁺	58.00	14.39	RIL-111	90.86	RIL-36	18.46	8.69
TW	N ⁰	1.76	1.02	RIL-96	2.58	RIL-70	0.32	0.25
	NO ₃ ⁻	1.77	0.97	RIL-125	2.99	RIL-59	0.33	0.25
	NH ₄ ⁺	1.76	1.00	RIL-102	2.65	RIL-70	0.33	9.69
GY	N ⁰	178.57	35.00	RIL-142	312.50	RIL-1	66.73	4.99
	NO ₃ ⁻	183.57	32.50	RIL-142	340.00	RIL-138	73.24	5.41
	NH ₄ ⁺	178.29	35.00	RIL-125	345.00	RIL-138	76.90	10.69

N-Forms of Nitrogen. **DF**-Days to 50% flowering; **PHSD**-Plant height at seedling (cm); **CCSD and CCFW**-SPAD reading at seedling and flowering stage, respectively; **PHMT**-Plant height at maturity (cm); **PL**-Panicle length (cm); **SPP**-Number of spikelet per panicle; **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²).

The character panicle length ranged from 18.80 to 30.60, 19.40 to 32.50 and 21.10 to 33.80 cm with mean value of 24.86, 25.52 and 26 cm under N^0 , NO_3^- and NH_4^+ respectively. The number of spikelets per panicle ranged from 33 to 303 with mean of 122.45 under N^0 , under NO_3^- it ranged for 46.33 to 219.33 with mean of 123.26 and under NH_4^+ condition 46.33 to 197.33 with mean of 122.01. The character number of filled grains per panicle ranged from 11.33 to 203.33 with mean of 73.24 whereas it ranged from 7 to 124.50 and 13.33 to 129.67 with mean of 72.68 and 70.82 under NO_3^- and NH_4^+ conditions respectively.

Under N^0 spikelet fertility ranged from 16.37 to 90.74 per cent with average of 59.74 per cent while under NO_3^- it varied from 11.67 to 86.55 per cent with average of 58.80 per cent and under NH_4^+ it ranged from 14.39 to 90.86 per cent with overall mean of 58 per cent. The phenotypic value for the trait test weight under N^0 ranged from 1.02 to 2.58 g with mean of 1.76 g, under NO_3^- it ranged from 0.97 to 2.99 g with overall mean of 1.77 g and under NH_4^+ it varied from 1 to 2.65 g with mean of 1.76 g. The grain yield ranged from 35 to 312.50 g/m^2 with overall mean phenotypic value of 178.57 g/m^2 under N^0 whereas under NO_3^- grain yield ranged from 32.50 to 340 g/m^2 with mean of 183.57 g/m^2 and under NH_4^+ it ranged from 35 to 345 g/m^2 with mean of 178.29 g/m^2 .

4.1.3 Yield responsiveness of selected rice genotypes

Adjusted mean yield performance, potential change in yield of a genotype with respect to all other tested genotypes and variation in yield over N^0 , NO_3^- and NH_4^+ treatment under aerobic condition during wet season 2015 is depicted in Appendices- E, F and G respectively. With the estimation of these parameters, genotypes can be classified into NH_4^+ or NO_3^- efficient genotype. Based on grain yield performance, top 10 genotypes under N^0 treatment, top 15 genotypes each under NO_3^- and NH_4^+ treatment were selected for further NUE study (Table 4.4). These genotypes showed drastic changes in grain yield amongst other genotypes under study. Similar Gonzalez-Dugo *et al.* (2005) reported the variability in resulting N status in two forage species displaying contrasting growth rates, yield and root

architecture when water and N are both limited. Genotypic differences in response to nitrogen fertilizers and nitrogen utilization have been previously reported by Broadbent *et al.*, 1987; Cho and Koh, 2005; De Datta and Broadbent, 1990; Park and Mok, 1975 and Seo *et al.*, 2005.

Among these, genotype Digamber Dhan, R-RF 105 and R-RHZ-2 yielded better over differential nitrogen treatment. These genotypes also showed near or high adjusted mean value for grain yield over high yielding checks *viz*; Samleshwari, Danteshwari and Indira Aerobic-1 and also hybrid Indira Sona.

Table: 4.4 List of selected genotypes based on grain yield under different nitrogen regimes for aerobic conditions along with their ranking during wet season 2015

Under N ⁰ N	R	Under NO ₃ ⁻ N	R	Under NH ₄ ⁺ N	R
Digamber Dhan (356.5)	1	R-RHZ-2 (361.9)	1	Dadhmaini Dhan (391.3)	1
R 1570-2644-2-1547-1 (302.9)	2	RP 5125-2-4 (347.5)	2	CGR-547 (Bargi) (361.8)	2
Dadhmaini dhan (324.0)	3	R-RF 105 (339.4)	3	Digamber Dhan (385.0)	3
R-RF 105 (271.6)	4	RCPR 8 (309.3)	4	R-RF 105 (320.7)	4
CR 3631-1-3 (282.9)	5	R 1860-783-1-424-1 (304.3)	5	IR 83376-B-B-110-3 (301.8)	5
R 1670-3269-2-3926-1 (265.4)	6	IR 84887-B-15 (292.5)	6	R 1672-1171-1-124-1 (300.5)	6
CR Dhan 40 (276.6)	7	Digamber Dhan (299.8)	7	R-RHZ-2 (310.7)	7
R-RHZ-2 (247.9)	8	R 2093-1536-1-660-1 (272.5)	8	R 1882-306-4-243-1 (285.5)	8
R 1432-251-103-1-1 (244.1)	9	R 1779-321-1-112-1 (268.7)	9	CR 3632-1-2 (328.2)	9
R 1902-912-2-512-1 (234.1)	10	CR Dhan 40 (280.5)	10	R 1860-783-1-424-1 (323.2)	10
		CGR-547 (Bargi) (265.3)	11	CR 3634-1-3 (319.5)	11
		R 1700-309-1-171-1 (267.5)	12	IR 84887-B-15 (270.5)	12
		RAU 1484-Aer-04 (271.8)	13	RCPR 8 (314.5)	13
		R 1570-2644-2-1547-1 (260.7)	14	R 1262-1667-1-1 (305.7)	14
		Dadhmaini Dhan (267.3)	15	R 1902-912-2-512-1 (277.0)	15
CD at 1% 114.16		CD at 1% 161.85		CD at 1% 147.92	
CD at 5% 84.06		CD at 5% 119.19		CD at 5% 108.93	

The data in parenthesis are their respective adjusted mean value of grain yield g/m²; R-Rank.

Grain yield accompanied by acceptable NUE is targeted in present research. Genotype (G), Environment (E), Nitrogen (N) and their interaction (GEN) play a profound & crucial role in the final expression of grain yield attributes. Considering this, on grain yield basis out of 85 lines, 25 lines along with seven checks and 6 additional lines *viz*; MTU-1010, CR Dhan 201, CR Dhan 202, IR-64, Indira Barani Dhan 1 and Sampada were selected further for assessing genotypic variability among rice genotypes for NUE and N-related traits. In another set 32 out of 179 RILs were selected on the basis of grain yield, the mean performance of these selected lines are

presented in Appendix-H and top ten lines along with their grain yield under differential N regimes is presented in Table 4.5. These 32 lines along with their parent are used for further single marker analysis.

Table: 4.5 Top ten lines among 32 selected RILs based on grain yield under different nitrogen regimes for aerobic conditions during wet season 2015

Rank	Under N^0N		Under NO_3^-N		Under NH_4^+N	
	Entry	Grain yield g/m^2	Entry	Grain yield g/m^2	Entry	Grain yield g/m^2
1	RIL-1	312.5	RIL-138	340.0	RIL-138	345.0
2	RIL-134	307.5	RIL-1	335.0	RIL-70	340.0
3	RIL-138	305.0	RIL-33	335.0	RIL-3	330.0
4	RIL-33	302.5	RIL-164	320.0	RIL-33	330.0
5	RIL-3	300.0	RIL-70	312.5	RIL-1	315.0
6	RIL-115	300.0	RIL-134	312.5	RIL-134	315.0
7	RIL-169	285.0	RIL-169	312.5	RIL-112	312.5
8	RIL-36	275.0	RIL-115	307.5	RIL-172	312.5
9	RIL-70	275.0	RIL-172	305.0	RIL-115	305.0
10	RIL-112	275.0	RIL-3	295.0	RIL-169	305.0

4.2 Analysis of variance for factorial design (wet season 2016)

The selected population was evaluated under wet season 2016 for various phenological, agronomical and physiological traits under different form of nitrogen i.e. zero nitrogen (N^0), Nitrogen in the form of calcium nitrate (NO_3^-) and Nitrogen in the form of ammonium chloride (NH_4^+) for both aerobic and anaerobic conditions. The experiment was conducted in three way factorial design. The mean data of individual lines of the population were statistically analyzed to generate overall mean and other genetic parameters. The results for factorial analysis of wet season 2016 for grain yield traits and NUE traits are presented in Tables 4.6 and 4.7 respectively. Analysis of variance (ANOVA) showed significant effect for all variance components genotype (G), nitrogen (N), environment (E) and their respective interactions *i.e.* genotype x nitrogen (GN), genotype x environment (EG), environment x nitrogen (EN), environment x nitrogen x genotype (ENG) for yield and majority of yield related traits in both seasons.

Table: 4.6 Analysis of variance for comparison of 38 selected germplasm accessions under N^0 , NO_3^- and NH_4^+ forms of nitrogen and variable environments for yield and yield related traits during wet season, 2016

Traits	Mean sum of Squares							Error
	G	N	E	G x N	G x E	E x N	G x N x E	
	DF= 37	DF= 2	DF= 1	DF= 74	DF= 37	DF= 2	DF= 74	DF= 277
DF	366.177**	29.928**	6.634	10.833**	29.152**	64.515**	7.425**	4.924
PHMT	1123.370**	7659.057**	44511.391**	48.009**	183.727**	2648.541**	56.268**	10.771
ET	0.936**	5.934**	6688.026**	0.718**	0.936**	5.932**	0.718**	0.201
PL	17.537**	51.79**	1158.244**	2.334**	4.978**	4.451**	2.227**	0.936
SPP	2023.097**	955.828**	201702.588**	442.732**	1276.521**	280.020	501.114**	102.235
FGP	1565.765**	605.421**	238935.486**	398.273**	1170.115**	759.247**	438.388**	85.831
SF	38.354**	11.248	7388.633**	20.671*	49.971**	152.934**	32.431**	14.230
TW	0.357**	0.300**	5.001**	0.049*	0.068**	0.092	0.055**	0.034
GY	35211.623**	117519.382**	9289808.460**	4781.272**	17886.137**	3787.520**	3841.637**	518.041
BY	439249.925**	4312488.954**	89690924.766**	30079.993**	171439.574**	261304.445**	30291.111**	7098.987
HI	273.922**	1167.494**	20.130	42.759**	182.730**	536.288**	36.871**	15.486

* and ** significance at .05, .01 levels respectively, **G**- Genotypes; **N**- Forms of nitrogen; **E**- Environments; **DF**-Days to 50% flowering; **PHMT**-Plant height at maturity (cm); **ET**-Effective tillers per plant; **PL**-Panicle length (cm); **SPP**-Number of spikelet per panicle; **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²); **BY**-Biological yield (g/m²) and **HI**-Harvest index (%).

Table: 4.7 Analysis of variance for comparison of 38 selected germplasm accessions under N^0 , NO_3^- and NH_4^+ forms of nitrogen and variable environments for NUE and its related traits during wet season, 2016

Traits	Mean sum of Squares							Error	
	G DF= 37	N DF= 2	E DF= 1	G x N DF= 74	G x E DF= 37	E x N DF= 2	G x N x E DF= 74	DF= 277	DF= 277
CCFW	37.552**	1245.906**	32.483**	10.358**	29.307**	188.803**	7.536**	4.724	4.724
GNC	0.137**	4.217**	13.353**	0.017**	0.030**	0.028**	0.017**	0.002	0.002
GPC	4.847**	149.162**	473.736**	0.597**	1.071**	0.993**	0.598**	0.088	0.088
SNC	0.064**	1.609**	7.367**	0.006**	0.021**	0.002	0.006**	0.002	0.002
GNV	8.229**	117.284**	625.179**	1.016**	2.914**	1.630**	0.680**	0.093	0.093
SNV	23.396**	583.040**	850.973**	2.270**	5.661**	2.298*	1.847**	0.537	0.537
BNV	45.062**	1223.268**	2934.503**	3.628**	9.656**	1.024	2.660**	0.588	0.588
NHI	415.254**	1389.220**	298.292**	64.850	263.772**	421.261**	54.886**	21.395	21.395
NUPE	0.007**	0.192**	0.455**	0.001**	0.001**	0.000	0.000**	0.000	0.000
NUtE	450.566**	8143.250**	13860.903**	57.674**	155.683**	42.090	43.968**	14.678	14.678
NUE	5.509**	18.369**	1451.597**	0.747**	2.796**	0.589**	0.600**	0.081	0.081

* and ** significance at .05, .01 levels respectively, **G**- Genotypes; **N**- Forms of nitrogen; **E**- Environments; **CCFW**- Chlorophyll content at flowering stage; **GNC**- Grain nitrogen content (%); **GPC**- Grain protein content (%); **SNC**- Straw nitrogen content (%); **GNV**- Grain nitrogen yield (g/m²); **SNV**- Straw nitrogen yield (g/m²); **BNV**- Biomass nitrogen yield (g/m²); **NHI**- Nitrogen harvest index (%); **NUPE**- Nitrogen uptake efficiency (gg⁻¹N); **NUtE**- Nitrogen utilization efficiency (gg⁻¹N) and **NUE**- Nitrogen use efficiency (gg⁻¹N).

Of all, ANOVA revealed significant differences among the genotypes for most of the traits studied ($p < 0.05$ & $p < 0.01$) indicating the presence of genetic variation among genotypes and possibility of manipulating these variations for improvement purposes. This is in accordance with the previous reports by Inthapanya *et al.* (2000), Tadesse *et al.* (2013) and Lakew (2015). Furthermore, genotype by nitrogen ($G \times N$) interaction and genotype by environment interaction (GXE), which was of main consideration in present research. The genotype by nitrogen ($G \times N$) interaction component was found significant for all traits under study except for nitrogen harvest index which imply non significant indicating the performance of genotypes were independent of the forms of N fertilizer. Similarly Fageria and Barbosa (2001) reported that grain yield, number of grains per panicle, 1000 grain weight, N uptake in grain, N harvest index and N use efficiency were significantly affected by genotype and N treatments.

4.2.1 Mean and variability parameters for yield and yield attributing traits

The mean phenotypic performance of grain yield and its traits are given in Table 4.8. In aerobic condition days to 50% flowering under N^0 condition ranged from 78 to 109 days with a mean of 91 days, under NO_3^- condition it ranged from 78 to 109 days with mean of 93 days and under NH_4^+ condition it varied from 78 to 111 days with mean of 92. In anaerobic condition under N^0 it ranged from 83 to 109 days with mean of 92 days, under NO_3^- condition it ranged from 83 to 110 days with the mean of 91 days, while under NH_4^+ condition it was ranged from 82 to 111 days with mean of 91 days.

In aerobic condition mean plant height at maturity under N^0 condition ranged from 68.77 to 103.17 cm with a mean of 81.36 cm, under NO_3^- condition it ranged from 76.27 to 111.70 cm with mean of 89.25 cm and under NH_4^+ condition it varied from 87.05 to 138.15 cm with mean of 103.60. In anaerobic condition under N^0 it ranged from 78.20 to 135.77 cm with mean of 108.70 cm, under NO_3^- condition it ranged from 78.67 to 141.18 cm with the mean of 110.38 cm, while under NH_4^+ condition it was ranged from 79.65 to 146.02 cm with mean of 114.40 cm.

In anaerobic condition number of effective tillers per plant varied from 6.17 to 8.83, 6.33 to 9.50 and 5.50 to 9.83 with average mean of 7.22, 7.76 and 8 under N^0 , NO_3^- and NH_4^+ respectively.

In aerobic condition under N^0 condition panicle length varied from 18.55 to 22.60 cm with average mean of 20.46 cm while in NO_3^- and NH_4^+ it ranged from 18.02 to 24.73 cm with mean of 20.93 cm and 19.23 to 24.05 cm with mean of 21.92 cm respectively. Whereas in anaerobic condition under N^0 panicle length ranged from 20.78 to 28.80 cm with mean of 23.99 cm, under NO_3^- condition it ranges from 19.17 to 30.05 cm with average mean of 24.11 cm while under NH_4^+ condition it varied from 20.67 to 30.33 cm with overall mean of 24.78 cm.

Under aerobic condition numbers of spikelets per panicle ranged from 83.50 to 126.33 with mean of 104.39 for N^0 condition while under NO_3^- condition mean numbers of spikelets per panicle was 104.38 and it ranged from 83.33 to 129.33 and under NH_4^+ condition it varied from 83 to 136.17 with average of 106.57. In anaerobic condition under N^0 condition mean numbers of spikelets per panicle ranges from 100.40 to 199.30 with mean of 146.59, while it was ranged from 99.90 to 197.10 with mean of 143.67 and 116 to 204.40 with mean of 151.26 under NO_3^- and NH_4^+ conditions respectively.

In aerobic condition numbers of filled grains per panicle varied from 63.33 to 108.33 with mean of 85 under N^0 condition while under NO_3^- and NH_4^+ conditions it ranged from 70.33 to 101.50 and 60 to 103.33 with overall mean of 84.11 and 84 respectively. Whereas in anaerobic condition mean of numbers of filled grains per panicle was 128.52, 127.01 and 134.92 under N^0 , NO_3^- and NH_4^+ respectively while it ranged from 90.20 to 175.70 under N^0 , 80.90 to 174.60 under NO_3^- and 99.30 to 182.20 under NH_4^+ .

Spikelet fertility ranged from 73.75 to 86.67 per cent under N^0 , 69.38 to 85.69 per cent under NO_3^- and 65.58 to 84.97 per cent under NH_4^+ condition for aerobic condition while overall mean of spikelet fertility was 81.26, 80.70 and 78.88 per cent under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition spikelet fertility ranged from 77.32 to 96.76 percent with mean of 87.69 per cent under N^0 , it ranged 80.49 to

96.12 per cent with mean of 88.19 per cent under NO_3^- and under NH_4^+ condition it varied from 82.36 to 95.60 per cent with average of 89.16 per cent.

In aerobic condition mean test weight under N^0 condition ranged from 1.74 to 2.73 g with a mean of 2.15 g, under NO_3^- condition it ranged from 1.77 to 2.79 g with mean of 2.25 g and under NH_4^+ condition it varied from 1.77 to 2.66 g with mean of 2.27g. In anaerobic condition under N^0 it ranged from 1.28 to 2.78 g with mean of 2.38 g, under NO_3^- condition it ranged from 1.99 to 2.91 g with the mean of 2.45 g, while under NH_4^+ condition it was ranged from 1.99 to 2.87 g with mean of 2.44 g.

Koffi *et al.* (2016b) reported that grain yield varied from genotype to genotype for N-P fertilizer. In aerobic condition the character grain yield ranged from 42.58 to 244.35 g/m^2 under N^0 , 58.30 to 278.82 g/m^2 under NO_3^- and 85.17 to 310.76 g/m^2 under NH_4^+ condition while overall mean of grain yield was 148.48, 186.70 and 213.12 g/m^2 under N^0 , NO_3^- and NH_4^+ respectively for aerobic condition. In anaerobic condition grain yield ranged from 247.39 to 618.47 g/m^2 with mean of 445.43 g/m^2 under N^0 condition, while it ranged 272.23 to 648.38 g/m^2 with mean of 467.38 g/m^2 under NO_3^- and under NH_4^+ condition it varied from 315 to 716.38 g/m^2 with average of 491.88 g/m^2 . Similar finding were also reported by Barraclough *et al.* (2010).

Under aerobic condition biological yield per plot ranged from 186.05 to 905.91 g/m^2 with overall mean of 450.58 g/m^2 for N^0 condition while under NO_3^- condition it varied from 313.80 to 1047.85 g/m^2 with mean of 665.24 g/m^2 and under NH_4^+ condition biological yield varied from 344.22 to 1317.04 g/m^2 with mean of 856.80 g/m^2 . Whereas in anaerobic condition biological yield under N^0 condition ranged from 713.27 to 1981.14 g/m^2 with average of 1433.29 g/m^2 , under NO_3^- condition it ranged from 832.91 to 2040.96 g/m^2 with mean of 1502.18 g/m^2 and under NH_4^+ condition it ranged from 857.75 to 2582.38 g/m^2 with mean of 1698.14 g/m^2 .

Harvest index ranged from 6.58 to 63.64 percent under N^0 , 7.22 to 52.48 percent under NO_3^- and 7.74 to 46.22 percent under NH_4^+ condition for aerobic condition with overall mean was 35.18, 29.47 and 26.16 percent under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition harvest index ranged from 22.25 to 41.94 percent with mean of 31.30 percent under N^0 , while under NO_3^- it ranged 17.90 to

43.39 percent with mean of 31.54 percent and under NH_4^+ condition it varied from 21.89 to 36.57 percent with average of 29.23 percent. Manzoor *et al.* (2006) and Chaturvedi (2005) reported that plant height, no. of productive tillers, panicle length, no. of grains per panicle, thousand grain weight and yield showed different trend with different N level. Similar finding were also reported by Rao *et al.* (2014).

In aerobic condition highest grain yield was reported by RP 5125-2-4 of 244.35, 278.82 and 310.76 g/m² under N^0 , NO_3^- and NH_4^+ respectively followed by IR-64 drought (227.11, 268.17 and 300.62 g/m²) and RAU 1484-Aer-04 (200.75, 241.31 and 262.60 g/m²). While two genotypes namely Swarna and Sampada reported lowest grain yield in aerobic condition.

In aerobic condition during wet season 2016 the highest plant height was reported by CGR-547 (Bargi) 101.65, 111.70 and 138.15 cm under N^0 , NO_3^- and NH_4^+ respectively followed by Basmati-370 (103.17, 105.12 and 112.87 cm) while genotypes R-1700-309-1-171-1, Sampada and Danteshwari reported lowest plant height of 68.77, 76.27 and 87.05 cm under N^0 , NO_3^- and NH_4^+ respectively.

The maximum panicle length was reported by Basmati-370 (22.60 cm) under N^0 and (24.73 cm) under NO_3^- and under NH_4^+ by CR Dhan-202 (24.05 cm) for aerobic condition. Whereas minimum panicle length was reported by Digamber Dhan (18.55 cm), Dadhmaini Dhan (18.02 cm) and Sampada (19.23 cm) under N^0 , NO_3^- and NH_4^+ respectively.

In aerobic maximum number of filled grains per panicle was reported by R-1882-306-4-243-1 (108.33) under N^0 , CR Dhan 40 (101.50) under NO_3^- and Sampada (103.33) under NH_4^+ while minimum was reported by R-1700-309-1-171-1 under N^0 (63.33) and NH_4^+ (60.00) and by IR 83376-B-B-110-3 (70.33) under NO_3^- .

In aerobic condition highest spikelet fertility was reported by CR-3632-1-2 (86.67%), R-1882-306-4-243-1 (85.81%) and R-1672-1171-1-124-1 (85.06%) under N^0 , genotypes R-1670-3269-2-3926-1 (85.69%) and Basmati-370 (85.01%) under NO_3^- whereas RAU 1484-Aer-04 (84.97%), R-1262-1667-1-1 (84.74%) and R-1670-3269-2-3926-1 (84.58%) reported maximum spikelet fertility under NH_4^+ for aerobic condition.

The genotypes namely Indira Sona, Indira Aerobic 1, Swarna, Basmati-370 and R-1779-321-1-112-1 reported highest biological yield under N^0 , NO_3^- and NH_4^+ for aerobic condition while genotype CR Dhan-40 showed lowest biological yield under all treatments for aerobic environments.

4.2.2 Mean and variability parameters for NUE and its attributing traits

The mean phenotypic performance of NUE and its traits are given in Table 4.9. In aerobic condition chlorophyll content varied from 24.86 to 40.18 with mean of 32.21 under N^0 condition while under NO_3^- and NH_4^+ conditions it ranged from 34 to 46.01 and 31.20 to 44.50 with overall mean of 38.67 and 38.26 respectively. Whereas in anaerobic condition mean of chlorophyll content was 33.53, 35.67 and 38.34 under N^0 , NO_3^- and NH_4^+ respectively while it ranged from 29.95 to 38.18 under N^0 , 32.40 to 40.40 under NO_3^- and 33.90 to 44.20 under NH_4^+ . Similarly Hassan *et al.* (2009) reported the genotypic variation in traditional rice varieties for chlorophyll content, SPAD value and nitrogen use efficiency. Islam *et al.* (2009) showed that chlorophyll content in leaves varies with varying rates of N applications. Similar finding was also reported by Konnerup and Brix (2010).

Grain nitrogen content ranged from 0.90 to 1.42 per cent under N^0 , 0.98 to 1.66 percent under NO_3^- and 1.02 to 1.77 percent under NH_4^+ condition for aerobic condition while overall mean of GNC was 1.21, 1.37 and 1.57 percent under N^0 , NO_3^- and NH_4^+ respectively. In anaerobic condition GNC ranged from 0.58 to 1.06 percent with mean of 0.90 percent under N^0 , while under NO_3^- it ranged 0.73 to 1.24 percent with mean of 1.03 percent and under NH_4^+ condition it varied from 0.88 to 1.62 percent with average of 1.20 percent.

In aerobic condition mean grain protein content under N^0 condition ranged from 5.37 to 8.45 percent with a mean of 7.22 percent, under NO_3^- condition it ranged from 5.83 to 9.87 percent with mean of 8.14 percent and under NH_4^+ condition it varied from 6.04 to 10.54 percent with mean of 9.36 percent. In anaerobic condition under N^0 GPC ranged from 3.46 to 6.33 percent with mean of 5.33 percent, under NO_3^- condition it ranged from 4.33 to 7.37 percent with the mean of 6.13 percent,

while under NH_4^+ condition it was ranged from 5.25 to 9.66 percent with mean of 7.14 percent. Similarly, Rao *et al.* (2014) also reported protein content of grain and available nitrogen were progressively augmented by incremental levels of N.

In aerobic condition the character straw nitrogen content ranged from 0.54 to 0.99 percent under N^0 , 0.61 to 1.17 percent under NO_3^- and 0.74 to 1.38 percent under NH_4^+ condition while overall mean of SNC was 0.82, 0.94 and 1.02 percent under N^0 , NO_3^- and NH_4^+ respectively for aerobic condition. In anaerobic condition straw nitrogen content ranged from 0.42 to 0.71 percent with mean of 0.56 percent under N^0 condition, while it ranged 0.50 to 0.83 percent with mean of 0.69 percent under NO_3^- and under NH_4^+ condition it varied from 0.63 to 0.88 percent with average of 0.77 percent.

In aerobic condition mean grain nitrogen yield under N^0 condition ranged from 0.55 to 3.11 g/m^2 with a mean of 1.81 g/m^2 , under NO_3^- condition it ranged from 0.80 to 4.39 g/m^2 with mean of 2.59 g/m^2 and under NH_4^+ condition it varied from 1.32 to 5.50 g/m^2 with mean of 3.38 g/m^2 . In anaerobic condition under N^0 it ranged from 1.77 to 6.52 g/m^2 with mean of 4.01 g/m^2 , under NO_3^- condition it ranged from 2.72 to 7.35 g/m^2 with the mean of 4.83 g/m^2 , while under NH_4^+ condition it was ranged from 3.43 to 9.26 g/m^2 with mean of 5.95 g/m^2 .

In aerobic condition straw nitrogen yield varied from 0.36 to 6.02 g/m^2 with mean of 2.52 g/m^2 under N^0 condition, while under NO_3^- and NH_4^+ conditions it ranged from 1.10 to 8.79 g/m^2 and 1.37 to 12.79 g/m^2 with overall mean of 4.53 g/m^2 and 6.67 g/m^2 respectively. Whereas in anaerobic condition mean of straw nitrogen yield was 5.53, 7.17 and 9.21 g/m^2 under N^0 , NO_3^- and NH_4^+ respectively while it ranged from 2.76 to 9.26 g/m^2 under N^0 , 2.97 to 11.42 g/m^2 under NO_3^- and 4.07 to 13.45 g/m^2 under NH_4^+ condition.

Under aerobic condition biological nitrogen yield per plot ranged from 1.43 to 8.08 g/m^2 with overall mean of 4.33 g/m^2 for N^0 condition while under NO_3^- condition it varied from 2.42 to 10.69 g/m^2 with mean of 7.11 g/m^2 and under NH_4^+ condition biological nitrogen yield varied from 2.98 to 15.07 g/m^2 with mean of 10.04 g/m^2 . Whereas in anaerobic condition biological nitrogen yield under N^0 condition ranged

from 4.53 to 14.44 g/m² with average of 9.54 g/m², under NO₃⁻ condition it ranged from 6.17 to 17.35 g/m² with mean of 12.0 g/m² and under NH₄⁺ condition it ranged from 7.94 to 21.98 g/m² with mean of 15.16 g/m². Results depicted differences in biomass N accumulation by Zhang *et al.* (2009).

Nitrogen harvest index ranged from 8.38 to 74.56 percent under N⁰, 8.38 to 64.0 percent under NO₃⁻ and 10.21 to 54.24 percent under NH₄⁺ condition for aerobic condition with overall mean was 44.17, 37.57 and 35.13 percent under N⁰, NO₃⁻ and NH₄⁺ respectively. In anaerobic condition nitrogen harvest index ranged from 32.59 to 53.65 percent with mean of 41.99 percent under N⁰, while under NO₃⁻ it ranged 22.09 to 51.95 percent with mean of 40.55 percent and under NH₄⁺ condition it varied from 29.76 to 49.05 percent with average of 39.18 percent. This finding was also reported by Barraclough *et al.* (2010).

In aerobic condition nitrogen uptake efficiency under N⁰ condition ranged from 0.02 to 0.10 gg⁻¹N with a mean of 0.05 gg⁻¹N, under NO₃⁻ condition it ranged from 0.03 to 0.13 gg⁻¹N with overall mean of 0.09 gg⁻¹N and under NH₄⁺ condition it varied from 0.04 to 0.19 gg⁻¹N with mean of 0.13 gg⁻¹N. In anaerobic condition under N⁰ it ranged from 0.06 to 0.18 gg⁻¹N with mean of 0.12 gg⁻¹N, under NO₃⁻ condition it ranged from 0.08 to 0.22 gg⁻¹N with the mean of 0.15 gg⁻¹N, while under NH₄⁺ condition it was ranged from 0.10 to 0.27 gg⁻¹N with mean of 0.19 gg⁻¹N. Similar Namai *et al.* (2009) found that wide variations in NUpE among rice varieties.

In aerobic condition under N⁰ condition nitrogen utilization efficiency varied from 6.53 to 82.58 gg⁻¹N with average mean of 36.96 gg⁻¹N while in NO₃⁻ and NH₄⁺ it ranged from 6.10 to 56.67 gg⁻¹N with mean of 27.60 gg⁻¹N and 5.95 to 53.59 gg⁻¹N with mean of 22.64 gg⁻¹N respectively. Whereas in anaerobic condition under N⁰ NUtE ranged from 32.21 to 71.83 gg⁻¹N with mean of 47.64 gg⁻¹N, under NO₃⁻ condition it ranges from 22.07 to 61.24 gg⁻¹N with average mean of 39.80 gg⁻¹N while under NH₄⁺ condition it varied from 23.23 to 41.41 gg⁻¹N with overall mean of 32.84 gg⁻¹N. Sattelmacher *et al.* (1994) pointed out that genotypes might differ in nitrogen use efficiency and uptake efficiency.

In aerobic condition mean nitrogen use efficiency under N^0 condition ranged from 0.53 to 3.05 $gg^{-1}N$ with a mean of 1.86 $gg^{-1}N$, under NO_3^- condition it ranged from 0.73 to 3.49 $gg^{-1}N$ with mean of 2.33 $gg^{-1}N$ and under NH_4^+ condition it varied from 1.06 to 3.88 $gg^{-1}N$ with mean of 2.66 $gg^{-1}N$. In anaerobic condition under N^0 it ranged from 3.09 to 7.73 $gg^{-1}N$ with mean of 5.57 $gg^{-1}N$, under NO_3^- condition it ranged from 3.40 to 8.10 $gg^{-1}N$ with the mean of 5.84 $gg^{-1}N$, while under NH_4^+ condition it was ranged from 3.94 to 8.95 $gg^{-1}N$ with mean of 6.15 $gg^{-1}N$.

Zhu *et al.* (2016) reported that the total N uptake values ranged from 138 to 208 $kg\ ha^{-1}$ in 2013 and from 150 to 248 $kg\ ha^{-1}$ in 2014. The N harvest index (NHI) ranged from 33.9 to 62.2% in 2013 and from 48.8 to 65.0% in 2014.

Genotypic differences in response to nitrogen fertilizers and nitrogen utilization have been previously reported by (Broadbent *et al.*, 1987; Cho and Koh, 2005; De Datta and Broadbent, 1990; Park and Mok, 1975; Seo *et al.*, 2005 and Hassan *et al.*, 2009). Abe *et al.* (2013) and Makhziah *et al.* (2013) reported significant genetic differences for grain yield (GY) and NUE components. Kang *et al.* (2013) reported that nitrogen uptake efficiency (NUpE) and nitrogen use efficiency (NUE) showed significant differences while harvest index (HI), nitrogen harvest index (NHI), and utilization efficiency (NUtE) didn't varied significantly by nitrogen fertilizer level.

In aerobic condition highest nitrogen use efficiency was reported by RP 5125-2-4 of 3.05, 3.49 and 3.88 $gg^{-1}N$ under N^0 , NO_3^- and NH_4^+ respectively followed by IR-64 Drought (2.84, 3.35 and 3.76 $gg^{-1}N$) and RAU 1484-Aer-04 (2.51, 3.02 and 3.28 $gg^{-1}N$). While two genotypes namely Swarna and Sampada reported lowest nitrogen use efficiency in aerobic condition.

The highest chlorophyll content was reported by R-1570-2644-2-1547-1 (40.18) under N^0 in aerobic condition while R-1672-1171-1-124-1 (46.01) and R 1779-321-1-112-1 (44.50) showed highest chlorophyll content under NO_3^- and NH_4^+ condition respectively. Whereas lowest chlorophyll content was reported by IR 64 under N^0 (24.98) and NH_4^+ (31.20) and by CR Dhan 202 (34.00) under NO_3^- for aerobic condition.

Table: 4.8 Mean phenotypic performance, genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance for yield and yield related traits of germplasm accessions under differential N regimes and environments during wet season, 2016

Traits	N	Aerobic/Rainfed Condition						Anaerobic/Irrigated Condition							
		Mean	Range		GCV	PCV	h ² (%)	GA as a % mean	Mean	Range		GCV	PCV	h ² (%)	GA as a % mean
			Min	Max						Min	Max				
DF	N ⁰	90.54	78.00	108.50	7.27	7.61	91.31	14.31	91.78	82.50	109.00	5.37	5.85	84.47	10.17
	NO ₃ ⁻	92.64	77.50	109.00	6.20	6.54	90.01	12.12	91.42	82.50	110.00	5.66	6.14	84.99	10.74
	NH ₄ ⁺	92.09	79.50	110.50	6.61	7.15	85.69	12.61	91.36	81.50	111.00	6.76	7.06	91.59	13.32
PHMT	N ⁰	81.36	68.77	103.17	10.11	11.16	82.06	18.87	108.70	78.20	135.77	11.00	11.19	96.75	22.29
	NO ₃ ⁻	89.25	76.27	111.70	8.91	9.86	81.69	16.59	110.38	78.67	141.18	11.90	12.04	97.81	24.25
	NH ₄ ⁺	103.60	87.05	138.15	9.87	10.61	86.42	18.89	114.40	79.65	146.02	11.58	11.85	95.58	23.33
ET	N ⁰	-	-	-	-	-	-	-	7.22	6.17	8.83	7.21	11.35	40.36	9.44
	NO ₃ ⁻	-	-	-	-	-	-	-	7.76	6.33	9.50	6.58	10.21	41.62	8.75
	NH ₄ ⁺	-	-	-	-	-	-	-	8.00	5.50	9.83	14.13	16.01	77.91	25.69
PL	N ⁰	20.46	18.55	22.60	4.49	6.36	49.86	6.53	23.99	20.78	28.80	7.87	9.09	74.90	14.03
	NO ₃ ⁻	20.93	18.02	24.73	5.48	7.22	57.73	8.58	24.11	19.17	30.05	7.55	8.49	79.02	13.82
	NH ₄ ⁺	21.92	19.23	24.05	4.58	6.12	56.07	7.07	24.78	20.67	30.33	7.08	7.86	81.04	13.12
SPP	N ⁰	104.39	83.50	126.33	7.07	10.30	47.12	10.00	146.59	100.40	199.30	20.00	21.18	89.19	38.92
	NO ₃ ⁻	104.38	83.83	129.33	8.53	11.59	54.13	12.92	143.67	99.90	197.10	16.71	18.38	82.72	31.32
	NH ₄ ⁺	106.57	83.00	136.17	9.05	13.27	46.57	12.73	151.26	116.00	204.40	16.81	18.15	85.77	32.08
FGP	N ⁰	85.00	63.33	108.33	9.05	12.74	50.43	13.24	128.52	90.20	175.70	20.26	21.63	87.74	39.09
	NO ₃ ⁻	84.11	70.33	101.50	8.04	11.70	47.24	11.39	127.01	80.90	174.60	18.54	19.96	86.33	35.49
	NH ₄ ⁺	84.00	60.00	103.33	10.15	14.46	49.24	14.67	134.92	99.30	182.20	17.60	19.01	85.68	33.56
SF	N ⁰	81.26	73.75	86.67	1.07	5.75	3.45	0.41	87.69	77.32	96.76	4.43	5.02	77.59	8.03
	NO ₃ ⁻	80.70	69.38	85.69	2.80	6.36	19.30	2.53	88.19	80.49	96.12	3.89	5.42	51.40	5.74
	NH ₄ ⁺	78.88	65.58	84.97	4.70	7.32	41.17	6.21	89.16	82.36	95.60	3.64	4.36	69.79	6.27
TW	N ⁰	2.15	1.74	2.73	8.92	11.22	63.22	14.61	2.38	1.28	2.78	7.50	16.38	20.95	7.07
	NO ₃ ⁻	2.25	1.77	2.79	9.22	11.72	61.85	14.93	2.45	1.99	2.91	8.53	11.15	58.50	13.44
	NH ₄ ⁺	2.27	1.77	2.66	8.61	11.18	59.33	13.66	2.44	1.99	2.87	6.37	10.36	37.73	8.06
GY	N ⁰	148.48	42.58	244.35	27.51	29.23	88.58	53.33	445.43	247.39	618.47	23.07	23.88	93.40	45.94
	NO ₃ ⁻	186.70	58.30	278.82	26.38	27.90	89.39	51.37	467.38	272.23	648.38	18.48	19.36	91.17	36.36
	NH ₄ ⁺	213.12	85.17	310.76	24.64	25.80	91.21	48.48	491.88	315.00	716.38	19.10	19.84	92.72	37.89
BY	N ⁰	450.58	186.05	905.91	30.78	32.84	87.85	59.42	1433.29	713.27	1981.14	20.83	21.86	90.85	40.90
	NO ₃ ⁻	665.24	313.80	1047.85	22.85	24.76	85.11	43.42	1502.18	832.91	2040.96	18.86	19.63	92.32	37.33
	NH ₄ ⁺	856.80	344.22	1317.04	21.45	23.89	80.58	39.66	1698.14	857.75	2582.38	18.84	19.31	95.14	37.85
HI	N ⁰	35.18	6.58	63.64	28.85	32.71	77.80	52.42	31.30	22.25	41.94	12.74	15.14	70.88	22.10
	NO ₃ ⁻	29.47	7.22	52.48	27.24	31.27	75.91	48.89	31.54	17.90	43.39	14.38	15.85	82.33	26.89
	NH ₄ ⁺	26.16	7.74	46.22	27.99	30.92	81.95	52.20	29.23	21.89	36.57	12.15	13.49	81.15	22.56
N- Forms of nitrogen; DF-Days to 50% flowering; PHMT-Plant height at maturity (cm); ET-Effective tillers per plant; PL-Panicle length (cm); SPP-Number of spikelets per panicle; FGP-Number of filled grains per panicle; SF-Spikelet fertility (%); TW-Test weight (g); GY-Grain yield (g/m ²); BY-Biological yield (g/m ²) and HI-Harvest index (%).															

N- Forms of nitrogen; **DF**-Days to 50% flowering; **PHMT**-Plant height at maturity (cm); **ET**-Effective tillers per plant; **PL**-Panicle length (cm); **SPP**-Number of spikelets per panicle; **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²); **BY**-Biological yield (g/m²) and **HI**-Harvest index (%).

Table: 4.9 Mean phenotypic performance, genotypic and phenotypic coefficient of variation, broad sense heritability and genetic advance for NUE and its related traits of germplasm accessions under differential N regimes and environments during wet season, 2016

Traits	N	Aerobic/Rainfed Condition					Anaerobic/Irrigated Condition				
		Mean	Range		PCV	h ² (%)	GA as a % mean	Range		PCV	h ² (%)
			Min	Max				Min	Max		
CCFW	N ⁰	32.21	24.86	40.18	10.94	13.30	67.68	18.54	33.53	29.95	38.18
	NO ₃ ⁻	38.67	34.00	46.01	6.89	7.95	75.16	12.31	35.67	32.40	40.40
	NH ₄ ⁺	38.26	31.20	44.50	7.43	9.67	59.10	11.77	38.34	33.90	44.20
GNC	N ⁰	1.21	0.90	1.42	9.46	10.04	88.74	18.36	0.90	0.58	1.06
	NO ₃ ⁻	1.37	0.98	1.66	10.69	11.27	89.98	20.89	1.03	0.73	1.24
	NH ₄ ⁺	1.57	1.02	1.77	10.44	11.02	89.81	20.38	1.20	0.88	1.62
GPC	N ⁰	7.22	5.37	8.45	9.46	10.04	88.74	18.36	5.33	3.46	6.33
	NO ₃ ⁻	8.14	5.83	9.87	10.69	11.27	89.98	20.89	6.13	4.33	7.37
	NH ₄ ⁺	9.36	6.04	10.54	10.44	11.02	89.81	20.38	7.14	5.25	9.66
SNC	N ⁰	0.82	0.54	0.99	13.19	13.85	90.71	25.88	0.56	0.42	0.71
	NO ₃ ⁻	0.94	0.61	1.17	10.74	11.45	87.94	20.75	0.69	0.50	0.83
	NH ₄ ⁺	1.02	0.74	1.38	12.41	12.80	94.00	24.79	0.77	0.63	0.88
GNY	N ⁰	1.81	0.55	3.11	31.31	33.01	89.97	61.18	4.01	1.77	6.52
	NO ₃ ⁻	2.59	0.80	4.39	33.18	34.69	91.51	65.39	4.83	2.72	7.35
	NH ₄ ⁺	3.38	1.32	5.50	29.17	30.45	91.76	57.55	5.95	3.43	9.26
SNY	N ⁰	2.52	0.36	6.02	46.79	50.39	86.22	89.50	5.53	2.76	9.26
	NO ₃ ⁻	4.53	1.10	8.79	33.48	36.61	83.64	63.08	7.17	2.97	11.42
	NH ₄ ⁺	6.67	1.37	12.79	34.24	36.86	86.26	65.50	9.21	4.07	13.45
BNY	N ⁰	4.33	1.43	8.08	32.32	34.19	89.32	62.92	9.54	4.53	14.44
	NO ₃ ⁻	7.11	2.42	10.69	24.31	26.20	86.06	46.45	12.00	6.17	17.35
	NH ₄ ⁺	10.04	2.98	15.07	25.01	26.66	87.99	48.33	15.16	7.94	21.98
NHI	N ⁰	44.17	8.38	74.56	25.85	29.44	77.12	46.77	41.99	32.59	53.65
	NO ₃ ⁻	37.57	8.38	64.00	26.61	29.64	80.59	49.21	40.55	22.09	51.95
	NH ₄ ⁺	35.13	10.21	54.24	27.30	29.58	85.21	51.92	39.18	29.76	49.05
NUpE	N ⁰	0.05	0.02	0.10	32.32	34.19	89.32	62.92	0.12	0.06	0.18
	NO ₃ ⁻	0.09	0.03	0.13	24.31	26.20	86.06	46.45	0.15	0.08	0.22
	NH ₄ ⁺	0.13	0.04	0.19	25.01	26.66	87.99	48.33	0.19	0.10	0.27
NUE	N ⁰	36.96	6.53	82.58	31.62	34.49	84.03	59.71	47.64	32.21	71.83
	NO ₃ ⁻	27.60	6.10	56.67	27.35	30.97	77.99	49.75	39.80	22.07	61.24
	NH ₄ ⁺	22.64	5.95	53.59	32.61	34.76	88.02	63.02	32.84	23.23	41.41
NUE	N ⁰	1.86	0.53	3.05	27.51	29.23	88.58	53.33	5.57	3.09	7.73
	NO ₃ ⁻	2.33	0.73	3.49	26.38	27.90	89.39	51.37	5.84	3.40	8.10
	NH ₄ ⁺	2.66	1.06	3.88	24.64	25.80	91.21	48.48	6.15	3.94	8.95

N- Forms of nitrogen; **CCFW**- Chlorophyll content at flowering stage; **GNC**- Grain nitrogen content (%); **GPC**- Grain protein content (%); **SNC**- Straw nitrogen content (%); **GNY**- Grain nitrogen yield (g/m²); **SNY**- Straw nitrogen yield (g/m²); **BNY**- Biomass nitrogen yield (g/m²); **NHI**- Nitrogen harvest index (%); **NUpE**- Nitrogen uptake efficiency (gg⁻¹N); **NUE**- Nitrogen utilization efficiency (gg⁻¹N) and **NUE**- Nitrogen use efficiency (gg⁻¹N).

RCPR 8, CR 3634-1-3 and RP 5125-2-4 were reported highest grain nitrogen and protein content under N^0 , NO_3^- and NH_4^+ for aerobic condition. The genotype R-1882-306-4-243-1 and CR 3631-1-3 also showed high grain nitrogen and protein content in rice grain. Whereas CR Dhan 40 reported lowest grain nitrogen and protein content in all treatment under aerobic condition.

The highest straw nitrogen content was reported by R-1882-306-4-243-1, Swarna and Samleshwari whereas lowest by CR Dhan 40 under N^0 , NO_3^- and NH_4^+ for aerobic condition. In aerobic the maximum nitrogen harvest index was reported by CR Dhan 40 (74.56% and 54.24%) under N^0 and NH_4^+ , CR 3631-1-3 (64.00%) under NO_3^- whereas Swarna and Sampada reported minimum nitrogen harvest index for all condition. The maximum nitrogen uptake was reported by Indira Sona of 0.10, 0.13 and 0.19 $gg^{-1}N$ under N^0 , NO_3^- and NH_4^+ for aerobic condition respectively and RAU 1484-Aer-04 reported maximum nitrogen uptake under NO_3^- (0.13 $gg^{-1}N$) and NH_4^+ condition whereas genotype CR dhan 40 was showed minimum nitrogen uptake for all conditions.

4.3 Variability studies

4.3.1 Phenotypic and genotypic co-efficient of variation (PCV and GCV)

The estimated values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters, under all conditions for both aerobic and anaerobic condition during wet season 2016 and are presented in Table 4.8 and Table 4.9. It clearly indicates that the apparent variation is not due to genotype but also due to the influence of environment. Comparative study of coefficient of variation on various characters revealed relatively high contribution of genotypic variation in determining the total phenotypic variation for most of the traits. Similarly Kumar *et al.* (2014) reported high PCV value than GCV for yield and yield contributing traits in rice.

In aerobic condition under N^0 the character plant height followed by chlorophyll content exhibited moderate value of GCV and PCV, while under NO_3^- and NH_4^+ condition these traits exhibited low value of GCV. Whereas character numbers

of filled grains per panicle exhibited moderate value of GCV coupled with PCV under NH_4^+ condition, while it exhibited low value of GCV but moderate value of PCV under N^0 and NO_3^- conditions. The traits namely grain nitrogen content and grain protein content exhibited moderate GCV and PCV value under both NO_3^- and NH_4^+ conditions whereas it depicted low GCV value but moderate PCV value under N^0 condition. The two traits namely numbers of seeds per panicle and test weight exhibited low GCV but moderate PCV value for under all conditions.

In anaerobic condition the trait plant height followed by numbers of seeds per panicle, numbers of filled grains per panicle, grain nitrogen content and grain protein content were exhibited moderate value of GCV and PCV under N^0 , NO_3^- and NH_4^+ conditions. Whereas character effective tillers per plant exhibited moderate value of PCV under N^0 , NO_3^- and NH_4^+ conditions.

The yield contributing traits like grain yield per plot, biological yield per plot and harvest index and NUE and its related traits namely straw nitrogen content, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake and utilization efficiency were exhibited moderate to high value of GCV under all conditions for both aerobic and anaerobic conditions. Only exception is that the trait straw nitrogen content depicted low GCV value under NH_4^+ for anaerobic condition. Similarly Tadesse *et al.* (2013) reported high phenotypic coefficient of variation (PCV) for Nitrogen uptake (UPE) (34.57%) and NUE (31.6%). They also suggest that the low heritability which makes selecting for traits difficult because environmental effect is more evident than genetic effect. Therefore future breeding efforts aim at exploiting the genetic variability available in the test genotypes.

Thus considering the value of GCV, PCV, h^2 and genetic advance, in present study under aerobic condition the traits namely grain yield followed by biological yield, harvest index, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency are the traits to have high values for the above said genetic parameters. Higher NUE has been observed in cultivars with higher grain harvest index (Bufogeles *et al.*, 1997). High heritability coupled with high genetic advance and

high GCV were earlier observed by Kumar *et al.* (2014) for the traits grain yield per plant, biological yield per plant and harvest index.

4.3.2 Heritability

Heritability is the heritable portion of the phenotypic variance. It is a good index of the transmission of characters from parents to offspring. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.*, 1955). The result of heritability for the traits under study of wet season 2016 is presented in Table 4.8 and Table 4.9.

The traits namely days to 50% flowering, plant height at maturity, grain yield, biological yield, harvest index, grain nitrogen content, grain protein content, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency were depicted high with more than 60 percent heritability under N^0 , NO_3^- and NH_4^+ for both aerobic and anaerobic conditions during wet season 2016. Similarly Babu *et al.* (2003) Singh *et al.* (2004) Kumar *et al.* (2008) Srinivasan *et al.* (2008) and Venuprasad *et al.* (2009) reported high heritability for grain yield and yield contributing traits. Makhziah *et al.* (2013) illustrated that heritability estimates (h^2) were high for most of measured traits at all N levels. This indicated that it is possible to select genotypes which are adapted to low N under both low and high N fertilization. High genotypic variation for grain yield was observed at all N levels, they also reported that reduction of N level from 180 to 90, 30 and 0 kg N.ha⁻¹ caused reduction of 7.8%, 14.4% and 49.4% grain yields respectively.

In aerobic condition traits namely panicle length, number of spikelets per panicle and number of filled grains per panicle exhibited moderate i.e. between 30 to 60 percent heritability under N^0 , NO_3^- and NH_4^+ conditions. Whereas in anaerobic condition these traits showed high i.e. more than 60 percent heritability under N^0 ,

NO_3^- and NH_4^+ conditions. Singh *et al.* (2004) also observed moderate heritability for panicle length.

The trait straw nitrogen content showed high heritability under all conditions for both aerobic and anaerobic conditions only exception is that it was showed moderate (52.78 %) heritability under NH_4^+ for anaerobic condition.

In aerobic condition the trait spikelet fertility showed low heritability under N^0 (3.45 %) and NO_3^- (19.30 %) while it showed moderate 41.17 % heritability under NH_4^+ condition. Test weight and chlorophyll content were depicted high heritability (63.22 % and 67.68 %) under N^0 and (61.85 % and 75.16 %) under NO_3^- conditions respectively, whereas showed moderate heritability for test weight (59.33 %) and chlorophyll content (59.10 %) under NH_4^+ condition.

In anaerobic condition number of effective tillers per plant and spikelets fertility showed moderate to high heritability under N^0 , NO_3^- and NH_4^+ conditions. Whereas two traits namely test weight and chlorophyll content was exhibited moderate heritability under N^0 , NO_3^- and NH_4^+ conditions. Similarly Masclaux-Daubresse (2011) reported that N concentration are robust traits, highly heritable, whereas GHI (grain harvest index) and NHI (nitrogen harvest index) are highly correlated and affected largely by N supply level and availability, particularly at the seed-filling stage. Lakew (2015) observed that the grain yield, harvest index, grain nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency had high genotypic and phenotypic coefficient of variation and high broad sense heritability estimates.

4.3.3 Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection and depends on three main factors (Allard, 1960). It is influenced by three factors i) the magnitude of genetic variability present among plants or families in base populations has important bearing on genetic advance. The greater the genetic variability the higher is the genetic advance and vice versa, ii) the heritability of the

character under consideration affects the genetic advance. The genetic advance is generally high with the character having high heritability and *vice versa* and iii) the proportion of plants or families selected for the study is called as selection intensity, which plays important role in the success of genetic advance. The selection intensity generally gives better results than low selection intensity.

The traits namely grain yield, biological yield, harvest index, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency were exhibited high value of genetic advance under all conditions for both aerobic and anaerobic conditions during wet season 2016. Whereas character days to 50% flowering showed moderate value of genetic advance under N^0 , NO_3^- and NH_4^+ for both aerobic and anaerobic conditions. The trait nitrogen harvest index showed moderate to high genetic advance under N^0 , NO_3^- and NH_4^+ for both aerobic and anaerobic conditions.

Under N^0 , NO_3^- and NH_4^+ the character plant height at maturity showed moderate value of genetic advance for aerobic while it showed high value of genetic advance for anaerobic condition. In anaerobic condition the character number of effective tillers per plant depicted low value of genetic advance under N^0 (9.44 %) and NO_3^- (8.75 %) while it showed high value of genetic advance under NH_4^+ (25.69 %).

Under N^0 , NO_3^- and NH_4^+ the character panicle length showed low value of genetic advance for aerobic while it showed moderate value of genetic advance for anaerobic condition. Whereas under N^0 , NO_3^- and NH_4^+ the traits number of spikelets per plant and number of filled grains per plant exhibited moderate and high value of genetic advance for aerobic and anaerobic condition respectively. Spikelet fertility showed low value of genetic advance for all condition.

In aerobic condition, test weight exhibited moderate value of genetic advance under N^0 , NO_3^- and NH_4^+ . Whereas in anaerobic condition it showed low value of genetic advance under N^0 and NH_4^+ while showed moderate genetic advance under NO_3^- .

Under N^0 , NO_3^- and NH_4^+ the character chlorophyll content showed moderate value of genetic advance for aerobic while it showed low value of genetic advance for anaerobic condition. The traits namely grain nitrogen content and grain protein content was showed moderate to high value of genetic advance under all conditions.

In aerobic condition under N^0 , NO_3^- and NH_4^+ the character straw nitrogen content exhibited high value of genetic advance. Whereas in anaerobic it showed moderate value of genetic advance under N^0 and NO_3^- while exhibited low value of genetic advance under NH_4^+ .

Kumar *et al.* (2014) suggested that the plant height, no. of effective tillers, leaf area index, vegetative plant growth and grain yield, these traits can be utilized as physiological markers for the selection of rice genotypes efficient in N-use. Huang *et al.* (2016) suggest that super-hybrid rice cultivar that achieves high grain yield by increasing harvest index and N-use efficiency.

Nandan *et al.* (2010) and Kiani (2013) reported high heritability coupled with high genetic advance found grain yield make this traits suitable for selection. In present study high heritability coupled with high genetic advance was recorded for plant height, grain yield, biological yield, harvest index, grain protein content, nitrogen harvest index, nitrogen uptake and nitrogen use efficiency. This indicated that these traits were predominantly controlled by additive gene action and more amenable for selection. Significant positive correlation of nitrogen use efficiency with grain was observed. Similar result was also reported by Naveen Kumar and Uma (2016). Karim *et al.* (2007) reported high heritability with high genetic advance for number of filled grains per panicle.

Shrivastava *et al.* (2014) reported that the traits viz., harvest index, biological yield per plant and plant height had high heritability accompanied with high genetic advance.

4.4 Association study

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables and is represented as 'r' in plant breeding, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. The path coefficient analysis was carried out by taking grain yield as separate and rest of the characters, as independent variables. The path coefficient analysis was used to partition the correlation coefficients of all the component characters studied with yield per plot, into direct and indirect effects.

4.4.1 Correlation analysis

In present study genotypic correlation between grain yield, yield attributing traits and NUE traits under different regimes of nitrogen and environmental conditions was evaluated at $P \leq 0.05$ and $P \leq 0.01$. The estimates of correlation for both environment and under N^0 , NO_3^- and NH_4^+ are presented in Tables 4.10.1, 4.10.2 and 4.10.3 respectively.

Harvest index followed by grain nitrogen yield, biological nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency and nitrogen use efficiency exhibited positive significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions over both i.e. aerobic and anaerobic conditions, similarly Frageria *et al.* (2011) reported that grain harvest index, N uptake and use efficiency in shoot and grain had significant positive association with grain yield. Prudente *et al.* (2008) reported higher correlations between the yield and N uptake of *japonica* and *indica* rice varieties. Similar finding were also reported by Sun *et al.* (2009) and Sun *et al.*, (2012). Jongdee *et al.* (1997) found that only biological yield and harvest index were found to be significantly associated with grain yield under drought treatments. Similar finding were also suggested by Babu *et al.* (2003) and Verulkar *et al.* (2004).

The trait biological yield had showed positive and significant correlation with grain yield in all environments exception for NH_4^+ for aerobic condition. This finding

is accordance with earlier by Umadevi *et al.*, 2009; Gomez *et al.*, 2010; Babu *et al.*, 2003 and Gomez *et al.*, 2006. Lanceras *et al.* (2004) reported that genetic improvement in the grain yield would likely be accompanied by improvement of biological yield.

Days to 50% flowering reported non-significant association with grain yield for all environments. Such correlation is also reported by Kumar *et al.* (2004) and Abarshahr *et al.* (2011).

In aerobic condition traits namely, plant height, panicle length and nitrogen utilization efficiency possessed positive and significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions. Gomez *et al.* (2006) reported positive and significant correlation of panicle length with grain yield under stress. Similar relation was also reported earlier in rice by Venuprasad *et al.* (2002). Frageria *et al.* (2011) also reported that plant height, shoot dry weight, grain harvest index, N uptake and use efficiency in shoot and grain had significant positive association with grain yield.

Whereas in anaerobic condition biological yield and straw nitrogen yield showed positive and significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions. Under well-watered conditions, Lanceras *et al.* (2004) also observed a high genetic association for biological yield, harvest index, plant height, and grain yield.

In anaerobic condition under N^0 chlorophyll content had showed positively significant correlation with grain yield whereas in rest of the conditions this trait showed non-significant correlation with grain yield. Similarly Tari *et al.* (2009) and Abarshahr *et al.* (2011) showed that the SPAD reading was positively correlated with rice yield that illustrated the importance of chlorophyll content and as it related to grain yield. Gopikannan and Ganesh (2013) reported significant positive association of grain yield per plant with total chlorophyll content and chlorophyll stability index. Similar finding was also reported by Islam *et al.* (2014).

In aerobic condition under N^0 grain nitrogen content was found non-significant with grain yield but showed positive significant association with grain yield

under NO_3^- and NH_4^+ conditions and straw nitrogen content had showed non-significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions.

In case of anaerobic condition grain nitrogen content and straw nitrogen content were showed non-significant association with grain yield under N^0 and NO_3^- conditions. Under NH_4^+ condition grain nitrogen content showed positive significant association with grain yield whereas trait straw nitrogen content had shown negative but significant correlation with grain yield. Lakew (2015) observed that the grain yield showed significant and positive correlation with grain nitrogen yield and nitrogen harvest index. Grain nitrogen concentration had significant and positive correlation with nitrogen uptake efficiency and nitrogen use efficiency.

In anaerobic condition the trait chlorophyll content showed positive and significant association with harvest index and grain nitrogen content under NH_4^+ . In aerobic condition chlorophyll content had shown negative but significant correlation with grain nitrogen content under N^0 , NO_3^- and NH_4^+ conditions. Straw nitrogen content showed positive significant correlation with chlorophyll content for N^0 and NO_3^- under anaerobic condition.

The traits namely harvest index, grain nitrogen yield, biological nitrogen yield, nitrogen harvest index and nitrogen uptake efficiency were showed positive and significant association with nitrogen use efficiency under N^0 , NO_3^- and NH_4^+ over both aerobic and anaerobic conditions. The character harvest index showed positive significant association with nitrogen harvest index under all variable environments this indicate that the character harvest index will be choose to improve nitrogen use efficiency.

In present study focus has to make for the selection of desirable traits particularly nitrogen related traits for improvement of grain yield. The characters Harvest index, grain nitrogen yield, biological nitrogen yield, nitrogen harvest index and nitrogen uptake efficiency were reflecting positive role for the improvement of nitrogen use efficient along with high grain yield genotypes. In aerobic condition traits namely, plant height, panicle length and nitrogen utilization efficiency possessed positive and significant association with grain yield under N^0 , NO_3^- and NH_4^+

Table: 4.10.1 Genotypic correlation between grain yield and NUE traits for N⁰ under aerobic and anaerobic condition

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNV	BNV	NHI	NUPE	NUtE	NUE	GY
DF	A	1.000	-0.024 ^{NS}	0.315 ^{**}	0.285 [*]	-0.404 ^{**}	-0.132 ^{NS}	0.234 [*]	0.333 ^{**}	-0.086 ^{NS}	0.393 ^{**}	0.296 ^{**}	-0.453 ^{**}	0.319 ^{**}	-0.468 ^{**}	-0.146 ^{NS}	-0.147 ^{NS}
	An	1.000	-0.065 ^{NS}	-0.006 ^{NS}	0.272 [*]	-0.490 ^{**}	-0.147 ^{NS}	0.270 [*]	0.039 ^{NS}	0.110 ^{NS}	0.372 [*]	0.274 [*]	-0.258 [*]	0.283 [*]	-0.467 ^{**}	-0.002 ^{NS}	-0.002 ^{NS}
PHMT	A		1.000	0.629 ^{**}	0.170 ^{NS}	0.203 ^{NS}	0.243 [*]	0.220 ^{NS}	0.287 [*]	0.303 ^{**}	0.204 ^{NS}	0.295 ^{**}	0.128 ^{NS}	0.283 [*]	0.080 ^{NS}	0.249 [*]	0.249 [*]
	An		1.000	0.678 ^{**}	0.452 ^{**}	-0.058 ^{NS}	0.251 [*]	-0.113 ^{NS}	-0.348 ^{**}	0.253 [*]	0.222 ^{NS}	0.256 [*]	0.071 ^{NS}	0.248 [*]	0.174 ^{NS}	0.407 ^{**}	0.407 ^{**}
PL	A			1.000	0.543 ^{**}	-0.210 ^{NS}	0.166 ^{NS}	0.177 ^{NS}	0.149 ^{NS}	0.296 ^{**}	0.514 ^{**}	0.553 ^{**}	-0.220 ^{NS}	0.540 ^{**}	-0.200 ^{NS}	0.287 [*]	0.287 [*]
	An			1.000	0.445 ^{**}	-0.013 ^{NS}	-0.107 ^{NS}	0.296 ^{**}	-0.009 ^{NS}	0.457 ^{**}	0.365 ^{**}	0.439 ^{**}	0.208 ^{NS}	0.435 ^{**}	-0.146 ^{NS}	0.410 ^{**}	0.410 ^{**}
BY	A				1.000	-0.559 ^{**}	-0.171 ^{NS}	0.293 [*]	0.260 [*]	0.451 ^{**}	0.914 ^{**}	0.953 ^{**}	-0.543 ^{**}	0.958 ^{**}	-0.582 ^{**}	0.425 ^{**}	0.426 ^{**}
	An				1.000	-0.137 ^{NS}	0.521 ^{**}	0.145 ^{NS}	-0.031 ^{NS}	0.732 ^{**}	0.873 ^{**}	0.875 ^{**}	0.011 ^{NS}	0.868 ^{**}	-0.140 ^{NS}	0.853 ^{**}	0.853 ^{**}
HI	A					1.000	0.126 ^{NS}	-0.239 [*]	-0.243 [*]	0.341 ^{**}	-0.734 ^{**}	-0.480 ^{**}	0.968 ^{**}	-0.488 ^{**}	0.914 ^{**}	0.434 ^{**}	0.433 ^{**}
	An					1.000	-0.086 ^{NS}	0.102 ^{NS}	0.286 [*]	0.377 ^{**}	-0.228 [*]	0.048 ^{NS}	0.871 ^{**}	0.043 ^{NS}	0.527 ^{**}	0.391 ^{**}	0.391 ^{**}
CCFW	A						1.000	-0.371 ^{**}	-0.095 ^{NS}	-0.189 ^{NS}	-0.138 ^{NS}	-0.192 ^{NS}	0.064 ^{NS}	-0.198 ^{NS}	0.194 ^{NS}	-0.096 ^{NS}	-0.097 ^{NS}
	An						1.000	0.145 ^{NS}	0.322 ^{**}	0.392 ^{**}	0.612 ^{**}	0.555 ^{**}	-0.115 ^{NS}	0.568 ^{**}	-0.304 ^{**}	0.446 ^{**}	0.446 ^{**}
GNC	A							1.000	0.614 ^{**}	0.468 ^{**}	0.360 ^{**}	0.494 ^{**}	-0.196 ^{NS}	0.468 ^{**}	-0.534 ^{**}	0.206 ^{NS}	0.206 ^{NS}
	An							1.000	0.704 ^{**}	0.623 ^{**}	0.420 ^{**}	0.552 ^{**}	0.416 ^{**}	0.567 ^{**}	-0.735 ^{**}	0.196 ^{NS}	0.196 ^{NS}
SNC	A								1.000	0.236 ^{**}	0.477 ^{**}	0.497 ^{**}	-0.403 ^{**}	0.492 ^{**}	-0.580 ^{**}	0.077 ^{NS}	0.078 ^{NS}
	An								1.000	0.393 ^{**}	0.425 ^{**}	0.425 ^{**}	0.226 [*]	0.440 ^{**}	-0.570 ^{**}	0.095 ^{NS}	0.095 ^{NS}
GVN	A									1.000	0.185 ^{NS}	0.561 ^{**}	0.368 ^{**}	0.534 ^{**}	0.103 ^{NS}	0.960 ^{**}	0.960 ^{**}
	An									1.000	0.712 ^{**}	0.909 ^{**}	0.600 ^{**}	0.908 ^{**}	-0.207 ^{NS}	0.883 ^{**}	0.883 ^{**}
SNV	A										1.000	0.917 ^{**}	-0.769 ^{**}	0.929 ^{**}	-0.775 ^{**}	0.106 ^{NS}	0.108 ^{NS}
	An										1.000	0.940 ^{**}	-0.117 ^{NS}	0.940 ^{**}	-0.515 ^{**}	0.676 ^{**}	0.676 ^{**}
BNV	A											1.000	-0.499 ^{**}	0.999 ^{**}	-0.611 ^{**}	0.478 ^{**}	0.479 ^{**}
	An											1.000	0.222 ^{NS}	0.999 ^{**}	-0.406 ^{**}	0.831 ^{**}	0.831 ^{**}
NHI	A												1.000	-0.512 ^{**}	0.922 ^{**}	0.450 ^{**}	0.448 ^{**}
	An												1.000	0.221 ^{NS}	0.290 [*]	0.481 ^{**}	0.481 ^{**}
NUPE	A													1.000	-0.610 ^{**}	0.458 ^{**}	0.459 ^{**}
	An													1.000	-0.423 ^{**}	0.823 ^{**}	0.823 ^{**}
NUtE	A														1.000	0.262 [*]	0.260 [*]
	An														1.000	0.149 ^{NS}	0.149 ^{NS}
NUE	A															1.000	1.000
	An															1.000	1.000
GY	A																1.000
	An																1.000

* and ** significance at .05 and .01 levels respectively, E- Environment; A- Aerobic; An-Anaerobic. DF-Days to 50% flowering; PHMT-Plant height at maturity (cm); PL- Panicle length (cm); ; BY-Biological yield (g/m²); HI-Harvest index (%). CCFW- Chlorophyll content at flowering stage; GNC- Grain nitrogen content (%); SNC- Straw nitrogen content (%); GNV- Grain nitrogen yield (g/m²); SNV- Biomass nitrogen yield (g/m²); BNV- Nitrogen harvest index (%); NHI- Nitrogen harvest index (%); NUPE- Nitrogen uptake efficiency (g g⁻¹N); NUtE- Nitrogen utilization efficiency (g g⁻¹N); NUE- Nitrogen use efficiency (g g⁻¹N) and GY-Grain yield (g/m²).

Table: 4.10.2 Genotypic correlation between grain yield and NUE traits for NO₃⁻ under aerobic and anaerobic condition

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNY	BNY	NHI	NUpE	NUE	NUE	GY
DF	A	1.000	-0.146 ^{NS}	0.252 [*]	0.478 ^{**}	-0.576 ^{**}	-0.043 ^{NS}	0.218 ^{NS}	0.489 ^{**}	-0.064 ^{NS}	0.635 ^{**}	0.524 ^{**}	-0.587 ^{**}	0.519 ^{**}	-0.722 ^{**}	-0.136 ^{NS}	-0.137 ^{NS}
	An	1.000	0.033 ^{NS}	0.146 ^{NS}	0.432 ^{**}	-0.384 ^{**}	0.035 ^{NS}	0.101 ^{NS}	0.206 ^{NS}	0.207 ^{NS}	0.520 ^{**}	0.461 ^{**}	-0.350 ^{**}	0.470 ^{**}	-0.413 ^{**}	0.163 ^{NS}	0.164 ^{NS}
PHMT	A	1.000	0.677 ^{**}	0.038 ^{NS}	0.241 [*]	0.146 ^{NS}	0.146 ^{NS}	0.106 ^{NS}	0.094 ^{NS}	0.265 [*]	0.023 ^{NS}	0.152 ^{NS}	0.203 ^{NS}	0.165 ^{NS}	0.204 ^{NS}	0.265 [*]	0.265 [*]
	An	1.000	0.442 ^{**}	0.105 ^{NS}	-0.181 ^{NS}	-0.181 ^{NS}	0.009 ^{NS}	-0.219 ^{NS}	0.022 ^{NS}	-0.084 ^{NS}	0.118 ^{NS}	0.042 ^{NS}	-0.238 [*]	0.049 ^{NS}	-0.101 ^{NS}	0.025 ^{NS}	0.025 ^{NS}
PL	A	1.000	1.000	0.557 ^{**}	-0.184 ^{**}	-0.184 ^{**}	0.190 ^{NS}	0.140 ^{NS}	0.065 ^{NS}	0.257 [*]	0.492 ^{**}	0.559 ^{**}	-0.160 ^{NS}	0.570 ^{**}	-0.200 ^{NS}	0.275 [*]	0.275 [*]
	An	1.000	1.000	0.371 ^{**}	-0.408 ^{**}	-0.408 ^{**}	-0.677 ^{**}	-0.105 ^{NS}	0.091 ^{NS}	0.027 ^{NS}	0.470 ^{**}	0.341 ^{**}	-0.411 ^{**}	0.322 ^{**}	-0.313 ^{**}	0.073 ^{NS}	0.072 ^{NS}
BY	A	1.000	1.000	1.000	-0.558 ^{**}	-0.558 ^{**}	0.095 ^{NS}	0.135 ^{NS}	0.185 ^{NS}	0.288 [*]	0.889 ^{**}	0.922 ^{**}	-0.507 ^{**}	0.921 ^{**}	-0.617 ^{**}	0.320 ^{**}	0.319 ^{**}
	An	1.000	1.000	1.000	-0.435 ^{**}	-0.435 ^{**}	0.328 ^{**}	0.216 ^{NS}	-0.078 ^{NS}	0.691 ^{**}	0.826 ^{**}	0.903 ^{**}	-0.215 ^{NS}	0.904 ^{**}	-0.363 ^{**}	0.743 ^{**}	0.744 ^{**}
HI	A	1.000	1.000	1.000	1.000	1.000	-0.115 ^{NS}	0.233 [*]	-0.135 ^{NS}	0.577 ^{**}	-0.767 ^{**}	-0.385 ^{**}	0.971 ^{**}	-0.374 ^{**}	0.880 ^{**}	0.585 ^{**}	0.585 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	-0.328 ^{**}	-0.077 ^{NS}	-0.224 ^{NS}	0.172 ^{NS}	-0.679 ^{**}	-0.393 ^{**}	0.866 ^{**}	-0.373 ^{**}	0.817 ^{**}	0.266 [*]	0.266 [*]
CCFW	A	1.000	1.000	1.000	1.000	1.000	1.000	-0.414 ^{**}	-0.381 ^{**}	-0.129 ^{NS}	0.003 ^{NS}	-0.061 ^{NS}	-0.115 ^{NS}	-0.067 ^{NS}	0.079 ^{NS}	-0.032 ^{NS}	-0.032 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	0.508 ^{**}	0.458 ^{**}	0.353 ^{**}	0.514 ^{**}	0.526 ^{**}	-0.211 ^{NS}	0.522 ^{**}	-0.554 ^{**}	0.178 ^{NS}	0.178 ^{NS}
GNC	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.503 ^{**}	0.665 ^{**}	0.112 ^{NS}	0.428 ^{**}	0.325 ^{**}	0.437 ^{**}	-0.156 ^{NS}	0.442 ^{**}	0.442 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.330 ^{**}	0.631 ^{**}	0.290 [*]	0.501 ^{**}	0.266 ^{**}	0.499 ^{**}	-0.491 ^{**}	0.189 ^{NS}	0.189 ^{NS}
SNC	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.180 ^{NS}	0.443 ^{**}	0.477 ^{**}	-0.251 [*]	0.474 ^{**}	-0.526 ^{**}	0.046 ^{NS}	0.045 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.021 ^{NS}	0.432 ^{**}	0.292 [*]	-0.430 ^{**}	0.289 [*]	-0.663 ^{**}	-0.214 ^{NS}	-0.214 ^{NS}
GNV	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.017 ^{NS}	0.482 ^{**}	0.627 ^{**}	0.498 ^{**}	0.283 ^{**}	0.963 ^{**}	0.963 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.437 ^{**}	0.778 ^{**}	0.447 ^{**}	0.788 ^{**}	-0.085 ^{NS}	0.877 ^{**}	0.877 ^{**}
SNY	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.868 ^{**}	-0.762 ^{**}	0.861 ^{**}	-0.840 ^{**}	-0.042 ^{NS}	-0.042 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.905 ^{**}	-0.587 ^{**}	0.897 ^{**}	-0.751 ^{**}	0.379 ^{**}	0.380 ^{**}
BNY	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.356 ^{**}	1.000 ^{**}	-0.596 ^{**}	0.442 ^{**}	0.441 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.198 ^{NS}	1.000 ^{**}	-0.565 ^{**}	0.680 ^{**}	0.680 ^{**}
NHI	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.342 ^{**}	0.872 ^{**}	0.613 ^{**}	0.613 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.182 ^{NS}	0.703 ^{**}	0.399 ^{**}	0.399 ^{**}
NUpE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.586 ^{**}	0.457 ^{**}	0.456 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.551 ^{**}	0.693 ^{**}	0.693 ^{**}
NUtE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.365 ^{**}	0.366 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.186 ^{NS}	0.187 ^{NS}
NUE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GY	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000

*** and **** significance at .05 and .01 levels respectively, **E**- Environment; **A**- Aerobic; **An**-Anaerobic. **DF**-Days to 50% flowering; **PHMT**-Plant height at maturity (cm); **PL**-Panicle length (cm); **BY**- Biological yield (g/m²); **HI**-Harvest index (%). **CCFW**- Chlorophyll content at flowering stage; **GNC**- Grain nitrogen content (%); **SNY**- Straw nitrogen content (%); **BNY**- Grain nitrogen yield (g/m²); **BNY**- Straw nitrogen yield (g/m²); **BNY**- Biomass nitrogen yield (g/m²); **NHI**- Nitrogen harvest index (%); **NUpE**- Nitrogen uptake efficiency (gg-1N); **NUtE**- Nitrogen utilization efficiency (gg-1N); **NUE**- Nitrogen use efficiency (gg-1N) and **GY**-Grain yield (g/m²).

Table: 4.10.3 Genotypic correlation between grain yield and NUE traits for NH_4^+ under aerobic and anaerobic condition

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNV	BNV	NHI	NUPE	NUE	NUE	GY
DF	A	1.000	-0.045 ^{NS}	0.147 ^{NS}	0.666 ^{**}	-0.670 ^{**}	-0.268 [*]	0.208 ^{NS}	0.446 ^{**}	-0.067 ^{NS}	0.741 ^{**}	0.647 ^{**}	-0.662 ^{**}	0.652 ^{**}	-0.686 ^{**}	-0.146 ^{NS}	-0.146 ^{NS}
	An	1.000	-0.008 ^{NS}	0.058 ^{NS}	0.341 ^{**}	-0.317 ^{**}	-0.142 ^{NS}	0.311 ^{**}	0.273 [*]	0.240 ^{**}	0.470 ^{**}	0.409 ^{**}	-0.171 ^{NS}	0.406 ^{**}	-0.469 ^{**}	0.143 ^{NS}	0.143 ^{NS}
PHMT	A	1.000	1.000	0.464 ^{**}	-0.016 ^{NS}	0.234 [*]	-0.010 ^{NS}	0.142 ^{NS}	0.104 ^{NS}	0.308 ^{**}	-0.059 ^{NS}	0.067 ^{NS}	0.206 ^{NS}	0.060 ^{NS}	0.116 ^{NS}	0.303 ^{**}	0.301 ^{**}
	An	1.000	1.000	0.494 ^{**}	0.478 ^{**}	-0.472 ^{**}	-0.244 [*]	0.010 ^{NS}	-0.034 ^{NS}	0.180 ^{NS}	0.547 ^{**}	0.426 ^{**}	-0.377 ^{**}	0.438 ^{**}	-0.382 ^{**}	0.210 ^{NS}	0.209 ^{NS}
PL	A	1.000	1.000	1.000	0.559 ^{**}	-0.052 ^{NS}	-0.028 ^{NS}	0.323 ^{**}	0.132 ^{NS}	0.503 ^{**}	0.363 ^{**}	0.528 ^{**}	-0.004 ^{NS}	0.517 ^{**}	-0.149 ^{NS}	0.486 ^{**}	0.486 ^{**}
	An	1.000	1.000	1.000	0.510 ^{**}	-0.497 ^{**}	-0.377 ^{**}	0.140 ^{NS}	-0.147 ^{NS}	0.215 ^{NS}	0.568 ^{**}	0.456 ^{**}	-0.294 ^{**}	0.462 ^{**}	-0.414 ^{**}	0.210 ^{NS}	0.210 ^{NS}
BY	A	1.000	1.000	1.000	1.000	-0.674 ^{**}	-0.215 ^{NS}	0.288 [*]	0.461 ^{**}	0.257 [*]	0.904 ^{**}	0.922 ^{**}	-0.652 ^{**}	0.928 ^{**}	-0.727 ^{**}	0.220 ^{NS}	0.220 ^{NS}
	An	1.000	1.000	1.000	1.000	-0.368 ^{**}	-0.043 ^{NS}	0.362 ^{**}	-0.255 [*]	0.750 ^{**}	0.923 ^{**}	0.942 ^{**}	-0.023 ^{NS}	0.946 ^{**}	-0.382 ^{**}	0.797 ^{**}	0.797 ^{**}
HI	A	1.000	1.000	1.000	1.000	1.000	0.249 [*]	-0.111 ^{NS}	-0.317 ^{**}	0.442 ^{**}	-0.777 ^{**}	-0.532 ^{**}	0.954 ^{**}	-0.540 ^{**}	0.919 ^{**}	0.530 ^{**}	0.530 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	0.394 ^{**}	0.031 ^{NS}	0.040 ^{NS}	0.200 ^{NS}	-0.564 ^{**}	-0.245 ^{**}	0.830 ^{**}	-0.259 [*]	0.833 ^{**}	0.259 [*]	0.259 [*]
CCFW	A	1.000	1.000	1.000	1.000	1.000	1.000	-0.482 ^{**}	-0.060 ^{NS}	-0.131 ^{NS}	-0.185 ^{NS}	-0.219 ^{NS}	0.107 ^{NS}	-0.211 ^{NS}	0.307 ^{**}	0.012 ^{NS}	0.012 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	0.425 ^{**}	-0.091 ^{NS}	0.343 ^{**}	-0.155 ^{NS}	0.077 ^{NS}	0.582 ^{**}	0.084 ^{NS}	0.184 ^{NS}	0.193 ^{NS}	0.193 ^{NS}
GNC	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.396 ^{**}	0.550 ^{**}	0.274 [*]	0.465 ^{**}	0.058 ^{NS}	0.467 ^{**}	-0.382 ^{**}	0.290 [*]	0.290 [*]
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.228 [*]	0.730 ^{**}	0.400 ^{**}	0.612 ^{**}	0.512 ^{**}	0.610 ^{**}	-0.435 ^{**}	0.375 ^{**}	0.374 ^{**}
SNC	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.258 [*]	0.697 ^{**}	0.734 ^{**}	-0.458 ^{**}	0.726 ^{**}	-0.582 ^{**}	0.151 ^{NS}	0.151 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.095 ^{NS}	0.060 ^{NS}	-0.011 ^{NS}	-0.121 ^{NS}	-0.025 ^{NS}	-0.358 ^{**}	-0.230 [*]	-0.231 [*]
GNV	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.029 ^{NS}	0.419 ^{**}	0.483 ^{**}	0.420 ^{**}	0.150 ^{NS}	0.956 ^{**}	0.956 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.606 ^{**}	0.873 ^{**}	0.600 ^{**}	0.869 ^{**}	-0.087 ^{NS}	0.905 ^{**}	0.905 ^{**}
SNV	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.920 ^{**}	-0.820 ^{**}	0.920 ^{**}	-0.837 ^{**}	-0.046 ^{NS}	-0.046 ^{NS}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.917 ^{**}	-0.254 [*]	0.920 ^{**}	-0.656 ^{**}	0.589 ^{**}	0.588 ^{**}
BNV	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.555 ^{**}	1.000 ^{**}	-0.701 ^{**}	0.333 ^{**}	0.333 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.146 ^{NS}	1.000 ^{**}	0.815 ^{**}	0.815 ^{**}	0.815 ^{**}
NHI	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.877 ^{**}	0.524 ^{**}	0.524 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.877 ^{**}	0.524 ^{**}	0.524 ^{**}
NUPE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.544 ^{**}	0.494 ^{**}	0.494 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.544 ^{**}	0.494 ^{**}	0.494 ^{**}
NUE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.709 ^{**}	0.333 ^{**}	0.333 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.709 ^{**}	0.333 ^{**}	0.333 ^{**}
NUE	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.810 ^{**}	0.809 ^{**}	0.809 ^{**}
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.810 ^{**}	0.809 ^{**}	0.809 ^{**}
GY	A	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.291 [*]	0.291 [*]
	An	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.142 ^{NS}	0.142 ^{NS}

***** and ****** significance at .05 and .01 levels respectively, **E**- Environment; **A**- Aerobic; **An**-Anaerobic. **DF**-Days to 50% flowering; **PHMT**-Plant height at maturity (cm); **PL**-Panicle length (cm); **BY**- Biological yield (g/m²); **HI**-Harvest index (%). **CCFW**- Chlorophyll content at flowering stage; **GNC**- Grain nitrogen content (%); **SNC**- Straw nitrogen content (%); **GNV**- Grain nitrogen yield (g/m²); **SNV**- Straw nitrogen yield (g/m²); **BNV**- Biomass nitrogen yield (g/m²); **NHI**- Nitrogen harvest index (%); **NUPE**- Nitrogen uptake efficiency (gg-1N) and **GY**-Grain yield (g/m²). **NUE**- Nitrogen use efficiency (gg-1N) and **GY**-Grain yield (g/m²).

conditions hence selection would be rewarding for those traits in particular environments. Samonte *et al.* (2006) reported that grain yield was positively correlated with NUE, N content and NTR, whereas NTR was correlated with grain protein concentration and suggested that the plant breeders could use these significant correlations to their advantage in breeding for rice cultivars that not only produce high yield but also utilize N efficiently and produce grain with a higher protein concentration. Zhu *et al.* (2016) reported that the both the total N uptake and NUE significantly contributed to the increased grain yield at $p < 0.01$ in 2013 and 2014.

4.4.2 Path analysis

The concept of path correlation coefficient was originally developed by Wright (1921) but the technique was used by Dewey and Lu (1959). The result of various causes influencing grain yield (direct effects) under N^0 , NO_3^- and NH_4^+ is shown in Tables 4.11.1, 4.11.2 and 4.11.3 respectively at the genotypic levels for all conditions.

In aerobic condition under N^0 the harvest index and nitrogen use efficiency were exhibiting high direct effect on grain yield. Biomass nitrogen yield exhibiting very high direct effect on grain yield. In anaerobic condition under N^0 two traits plant height and biological yield exhibited positive but negligible direct effect on grain yield. Whereas the characters grain nitrogen yield, straw nitrogen yield and nitrogen use efficiency were showed low, moderate and high direct effect on grain yield respectively. Similarly Nandan *et al.* (2010) reported positive direct effect on grain yield exhibited by the traits plant height and harvest index. Kumar *et al.* (2014) revealed that the traits such as plant height and days to heading exhibited significant positive correlation with grain yield per plant as well as positive direct effects on grain yield per plant.

Under NO_3^- condition trait, nitrogen harvest index exhibiting negligible direct effect on grain yield for both aerobic and anaerobic conditions. Whereas biomass nitrogen yield and nitrogen use efficiency depicted moderate and very high direct effects on grain yield respectively under NO_3^- over both aerobic and anaerobic conditions.

Under NH_4^+ for aerobic condition the characters, grain nitrogen content and straw nitrogen content showed moderate direct effect on grain yield. Trait harvest index under aerobic condition and nitrogen use efficiency for both conditions had shown high direct effect on grain yield. Biological yield and grain nitrogen yield exhibited very high direct effect on grain yield under NH_4^+ for aerobic condition. In anaerobic situation the traits namely biological yield, grain nitrogen content, straw nitrogen content, nitrogen harvest index and nitrogen uptake efficiency were exhibited positive but negligible direct effect on grain yield and two traits namely biomass nitrogen yield and nitrogen use efficiency were exhibiting respective low and very high direct effect on grain yield under NH_4^+ .

The characters Harvest index, grain nitrogen yield, biological nitrogen yield, nitrogen harvest index and nitrogen uptake efficiency were exhibit positive correlation along as well as showed direct effect on grain yield it reveals true relationship between them and direct selection for these traits will be rewarding for yield improvement. Zhu *et al.* (2016) suggested that genetic improvements in rice grain yield are associated with increased NUE.

Grain nitrogen content and straw nitrogen content exhibited negative correlation with grain yield under N^0 and NO_3^- for both aerobic and anaerobic conditions. Hence, under such situation direct selection for such traits should be practiced to reduce the undesirable indirect effects. Whereas, grain nitrogen content, grain nitrogen yield and straw nitrogen yield was the only traits to record high negative direct effect on grain yield under NH_4^+ for both aerobic and anaerobic condition. Low residual effect was obtained under all the condition at genotypic levels, indicating that factors which have been considered here are sufficient to contribute for yield. Kang *et al.* (2013) illustrate information on NUE variability and its relationships with yield and yield related traits in rice has led to investigation of genetic variability in N use efficiency among upland rice genotypes, identifying genotypes with best N use efficiency and also assessing nature of association among N use efficiency and yield and yield

Table: 4.11.1 Direct and Indirect effect of yield contributing and NUE traits upon grain yield for N⁰ under aerobic and anaerobic conditions

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNV	BNV	NHI	NUtE	NUE	r values of grain yield
DF	A	-0.008	0.000	0.000	-0.009	-0.235	0.001	0.016	-0.062	0.177	-1.743	1.626	0.266	0.035	-0.141	-0.147 ^{NS}
	An	0.000	0.000	0.000	0.003	-0.004	0.000	0.000	0.000	0.022	0.084	-0.109	0.002	0.002	-0.002	-0.002 ^{NS}
PHMT	A	0.000	-0.011	-0.001	-0.005	0.118	-0.002	0.015	-0.053	-0.622	-0.905	1.619	-0.075	-0.006	0.240	0.249 [*]
	An	0.000	0.002	-0.001	0.004	-0.001	0.000	0.000	0.000	0.050	0.050	-0.102	-0.001	-0.001	0.406	0.407 ^{**}
PL	A	-0.003	-0.007	-0.001	-0.016	-0.122	-0.001	0.012	-0.028	-0.608	-2.278	3.041	0.129	0.015	0.276	0.287 [*]
	An	0.000	0.001	-0.001	0.004	0.000	0.000	0.000	0.000	0.091	0.082	-0.175	-0.002	0.001	0.409	0.410 ^{**}
BY	A	-0.002	-0.002	-0.001	-0.030	-0.325	0.001	0.020	-0.048	-0.927	-4.054	5.236	0.319	0.043	0.409	0.426 ^{**}
	An	0.000	0.001	-0.001	0.010	-0.001	-0.001	0.000	0.000	0.146	0.196	-0.348	0.000	0.001	0.851	0.853 ^{**}
HI	A	0.003	-0.002	0.000	0.017	0.580	-0.001	-0.016	0.045	-0.700	3.255	-2.639	-0.569	-0.068	0.418	0.433 ^{**}
	An	0.000	0.000	0.000	-0.001	0.009	0.000	0.000	0.000	0.075	-0.051	-0.019	-0.008	-0.003	0.390	0.391 ^{**}
CCFW	A	0.001	-0.003	0.000	0.005	0.073	-0.008	-0.025	0.018	0.387	0.611	-1.055	-0.038	-0.014	-0.093	-0.097 ^{NS}
	An	0.000	0.000	0.000	0.005	-0.001	-0.001	0.000	0.000	0.078	0.138	-0.220	0.001	0.002	0.444	0.446 ^{**}
GNC	A	-0.002	-0.002	0.000	-0.009	-0.139	0.003	0.067	-0.114	-0.962	-1.599	2.714	0.115	-0.105	0.198	0.206 ^{NS}
	An	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.124	0.095	-0.220	-0.004	0.004	0.196	0.196 ^{NS}
SNC	A	-0.003	-0.003	0.000	-0.008	-0.141	0.001	0.041	-0.186	-0.484	-2.117	2.733	0.237	-0.110	0.075	0.078 ^{NS}
	An	0.000	-0.001	0.000	0.000	0.002	0.000	0.000	0.001	0.078	0.089	-0.169	-0.002	0.003	0.095	0.095 ^{NS}
GNV	A	0.001	-0.003	0.000	-0.014	0.198	0.002	0.032	-0.044	-2.054	-0.820	3.082	-0.217	-0.119	0.924	0.960 ^{**}
	An	0.000	0.000	-0.001	0.007	0.003	-0.001	0.000	0.000	0.199	0.160	-0.361	-0.006	0.001	0.881	0.883 ^{**}
SNV	A	-0.003	-0.002	-0.001	-0.028	-0.426	0.001	0.024	-0.089	-0.379	-4.436	5.041	0.452	-0.207	0.103	0.108 ^{NS}
	An	0.000	0.000	0.000	0.009	-0.002	-0.001	0.000	0.000	0.142	0.225	-0.374	0.001	0.003	0.674	0.676 ^{**}
BNV	A	-0.002	-0.003	-0.001	-0.029	-0.279	0.002	0.033	-0.092	-1.152	-4.069	5.495	0.293	-0.223	0.461	0.479 ^{**}
	An	0.000	0.000	-0.001	0.009	0.000	-0.001	0.000	0.000	0.181	0.211	-0.397	-0.002	0.002	0.829	0.831 ^{**}
NHI	A	0.004	-0.001	0.000	0.016	0.562	-0.001	-0.013	0.075	-0.757	3.413	-2.741	-0.588	-0.069	0.433	0.448 ^{**}
	An	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.119	-0.026	-0.088	-0.010	-0.002	0.480	0.481 ^{**}
NUtE	A	-0.003	-0.003	-0.001	-0.029	-0.283	0.002	0.032	-0.091	-1.097	-4.119	5.488	0.301	0.045	0.441	0.459 ^{**}
	An	0.000	0.000	-0.001	0.009	0.000	-0.001	0.000	0.000	0.181	0.211	-0.397	-0.002	0.002	0.821	0.823 ^{**}
NUtE	A	0.004	-0.001	0.000	0.018	0.531	-0.002	-0.036	0.108	-0.211	3.437	-3.359	-0.542	0.136	0.252	0.260 [*]
	An	0.000	0.000	0.000	-0.001	0.005	0.000	0.000	0.000	-0.041	-0.116	0.162	-0.003	-0.075	0.149	0.149 ^{NS}
NUE	A	0.001	-0.003	0.000	-0.013	0.252	0.001	0.014	-0.014	-1.971	-0.472	2.628	-0.264	-0.102	0.963	1.000 ^{**}
	An	0.000	0.001	-0.001	0.008	0.003	-0.001	0.000	0.000	0.176	0.152	-0.330	-0.005	-0.001	0.997	1.000 ^{**}

Residual effect (R) -0.00002 and (I) -0.00000. E- Environment; A- Aerobic; An-Anaerobic. DF-Days to 50% flowering; PHMT-Plant height at maturity (cm); PL-panicle length (cm); BY-Biological yield (g/m²); HI-Harvest index (%). CCFW-Chlorophyll content at flowering stage; GNC- Grain nitrogen content (%); SNC- Straw nitrogen content (%); GNV- Grain nitrogen yield (g/m²); SNV- Biomass nitrogen yield (g/m²); BNV- Nitrogen harvest index (%); NHI- Nitrogen harvest index (%); NUtE- Nitrogen uptake efficiency (gg-IN); NHI- Nitrogen use efficiency (gg-IN) and NUE- Nitrogen use efficiency (gg-IN).

Table: 4.11.2 Direct and indirect effect of yield contributing and NUE traits upon grain yield for NO_3^- under aerobic and anaerobic conditions

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNV	BNV	NHI	NUPE	NUtE	NUE	r values of grain yield
DF	A	0.003	0.000	0.001	0.009	0.039	0.000	-0.008	0.012	0.024	-0.472	0.426	-0.055	0.008	0.007	-0.131	-0.137 ^{NS}
	An	0.000	0.000	0.000	0.000	-0.002	0.000	-0.001	-0.001	-0.026	-0.099	0.134	-0.003	-0.003	0.003	0.162	0.164 ^{NS}
PHMT	A	0.000	0.001	0.001	0.001	-0.017	0.000	-0.004	0.002	-0.101	-0.017	0.124	0.019	0.002	-0.002	0.255	0.265 [*]
	An	0.000	0.000	-0.001	0.000	-0.001	0.000	0.002	0.000	0.011	-0.023	0.012	-0.002	0.000	0.001	0.025	0.025 ^{NS}
PL	A	0.001	0.001	0.002	0.011	0.013	0.000	-0.005	0.002	-0.098	-0.365	0.455	-0.015	0.008	0.002	0.265	0.275 [*]
	An	0.000	0.000	-0.002	0.000	-0.002	0.000	0.001	0.000	-0.003	-0.090	0.099	-0.003	-0.002	0.003	0.072	0.072 ^{NS}
BY	A	0.001	0.000	0.001	0.019	0.038	0.000	-0.005	0.004	-0.110	-0.661	0.750	-0.047	0.013	0.006	0.308	0.319 ^{**}
	An	0.000	0.000	-0.001	-0.001	-0.002	0.000	-0.002	0.000	-0.088	-0.158	0.262	-0.002	-0.005	0.003	0.736	0.744 ^{**}
HI	A	-0.002	0.000	0.000	-0.011	-0.068	0.000	-0.008	-0.003	-0.220	0.570	-0.313	0.091	-0.005	-0.008	0.564	0.585 ^{**}
	An	0.000	0.000	0.001	0.000	0.004	0.000	0.001	0.001	-0.022	0.130	-0.114	0.006	0.002	-0.007	0.263	0.266 [*]
CCFW	A	0.000	0.000	0.000	0.002	0.008	-0.001	0.014	-0.009	0.049	-0.002	-0.050	-0.011	-0.001	-0.001	-0.031	-0.032 ^{NS}
	An	0.000	0.000	0.001	0.000	-0.001	-0.001	-0.005	-0.002	-0.045	-0.098	0.153	-0.002	-0.003	0.005	0.176	0.176 ^{NS}
GNC	A	0.001	0.000	0.000	0.003	-0.016	0.001	-0.035	0.012	-0.253	-0.083	0.348	0.030	0.006	0.001	0.426	0.442 ^{**}
	An	0.000	0.000	0.000	0.000	0.000	0.000	-0.009	-0.001	-0.080	-0.055	0.145	0.002	-0.003	0.004	0.188	0.189 ^{NS}
SNC	A	0.001	0.000	0.000	0.004	0.009	0.001	-0.018	0.024	-0.069	-0.329	0.388	-0.023	0.007	0.005	0.045	0.045 ^{NS}
	An	0.000	0.000	0.000	0.000	-0.001	0.000	-0.003	-0.003	0.003	-0.082	0.085	-0.003	-0.002	0.006	-0.212	-0.214 ^{NS}
GNV	A	0.000	0.000	0.001	0.005	-0.039	0.000	-0.023	0.004	-0.381	0.013	0.392	0.058	0.007	-0.003	0.928	0.963 ^{**}
	An	0.000	0.000	0.000	-0.001	0.001	0.000	-0.006	0.000	-0.127	-0.083	0.226	0.003	-0.005	0.001	0.869	0.877 ^{**}
SNV	A	0.002	0.000	0.001	0.017	0.052	0.000	-0.004	0.011	0.006	-0.743	0.706	-0.071	0.012	0.008	-0.040	-0.042 ^{NS}
	An	0.000	0.000	-0.001	-0.001	-0.003	0.000	-0.003	-0.002	-0.056	-0.191	0.263	-0.004	-0.005	0.006	0.376	0.380 ^{**}
BNV	A	0.002	0.000	0.001	0.017	0.026	0.000	-0.015	0.011	-0.183	-0.645	0.813	-0.033	0.015	0.006	0.426	0.441 ^{**}
	An	0.000	0.000	-0.001	-0.001	-0.002	0.000	-0.005	-0.001	-0.099	-0.173	0.290	-0.001	-0.006	0.005	0.673	0.680 ^{**}
NHI	A	-0.002	0.000	0.000	-0.010	-0.066	0.000	-0.011	-0.006	-0.239	0.566	-0.290	0.093	-0.005	-0.008	0.590	0.613 ^{**}
	An	0.000	0.000	0.001	0.000	0.004	0.000	-0.002	0.001	-0.057	0.112	-0.058	0.007	0.001	-0.006	0.395	0.399 ^{**}
NUPE	A	0.002	0.000	0.001	0.017	0.026	0.000	-0.015	0.011	-0.189	-0.640	0.814	-0.032	0.015	0.005	0.441	0.456 ^{**}
	An	0.000	0.000	-0.001	-0.001	-0.002	0.000	-0.005	-0.001	-0.100	-0.171	0.290	-0.001	-0.006	0.005	0.686	0.693 ^{**}
NUtE	A	-0.002	0.000	0.000	-0.012	-0.060	0.000	0.005	-0.013	-0.108	0.624	-0.484	0.081	-0.009	-0.009	0.352	0.366 ^{**}
	An	0.000	0.000	0.001	0.000	0.003	0.000	0.005	0.002	0.011	0.143	-0.164	0.005	0.003	-0.008	0.185	0.187 ^{NS}
NUE	A	0.000	0.000	0.001	0.006	-0.040	0.000	-0.015	0.001	-0.366	0.031	0.359	0.057	0.007	-0.003	0.964	1.000 ^{**}
	An	0.000	0.000	0.000	-0.001	0.001	0.000	-0.002	0.001	-0.112	-0.072	0.197	0.003	-0.004	-0.002	0.990	1.000 ^{**}

Residual Effect (R) -0.00001 and (I) -0.00000. E- Environment; A- Aerobic; An-Anaerobic. DF-Days to 50% flowering; PHMT-Plant height at maturity (cm); PL-panicle length (cm); BY-Biological yield (g/m²); HI-Harvest index (%). CCFW- Chlorophyll content at flowering stage; GNC- Grain nitrogen content (%); SNC- Straw nitrogen content (%); GNV- Grain nitrogen yield (g/m²); SNV- Straw nitrogen yield (g/m²); BNV- Biomass nitrogen yield (g/m²); NHI- Nitrogen harvest index (%); NUPE- Nitrogen uptake efficiency (gg-1N); NUtE- Nitrogen utilization efficiency (gg-1N) and NUE- Nitrogen use efficiency (gg-1N).

Table: 4.11.3 Direct and indirect effect of yield contributing and NUE traits upon grain yield for NH_4^+ under aerobic and anaerobic conditions

Traits	E	DF	PHMT	PL	BY	HI	CCFW	GNC	SNC	GNV	SNV	BNV	NHI	NUPE	NUtE	NUE	r values of grain yield
DF	A	0.029	0.001	-0.004	0.753	-0.527	-0.001	0.045	0.118	-2.211	56.206	-53.918	0.384	-0.884	-0.030	-0.105	-0.146 ^{NS}
	An	0.001	0.000	0.000	0.009	0.006	0.000	0.006	0.003	-0.037	-0.084	0.076	0.000	0.023	-0.007	0.146	0.143 ^{NS}
PHMT	A	-0.001	-0.013	-0.013	-0.018	0.184	0.000	0.031	0.027	10.140	-4.479	-5.578	-0.119	-0.082	0.005	0.218	0.301 ^{**}
	An	0.000	0.000	0.000	0.013	0.009	0.000	0.000	0.000	-0.028	-0.098	0.079	0.000	0.025	-0.006	0.214	0.209 ^{NS}
PL	A	0.004	-0.006	-0.029	0.632	-0.041	0.000	0.070	0.035	16.580	27.552	-43.955	0.002	-0.701	-0.007	0.349	0.486 ^{**}
	An	0.000	0.000	0.001	0.014	0.009	0.000	0.003	-0.002	-0.033	-0.101	0.084	0.000	0.027	-0.006	0.215	0.210 ^{NS}
BY	A	0.019	0.000	-0.016	1.132	-0.530	-0.001	0.062	0.122	8.481	68.529	-76.823	0.377	-1.258	-0.032	0.158	0.220 ^{NS}
	An	0.000	0.000	0.000	0.027	0.007	0.000	0.007	-0.003	-0.115	-0.165	0.174	0.000	0.055	-0.006	0.815	0.797 ^{**}
HI	A	-0.019	-0.003	0.002	-0.763	0.786	0.001	-0.024	-0.084	14.582	-58.879	44.330	-0.552	0.732	0.041	0.381	0.530 ^{**}
	An	0.000	0.000	0.000	-0.010	-0.019	0.000	0.001	0.000	-0.031	0.101	-0.045	0.001	-0.015	0.012	0.265	0.259 [*]
CCFW	A	-0.008	0.000	0.001	-0.244	0.196	0.005	-0.104	-0.016	-4.304	-14.008	18.248	-0.062	0.287	0.014	0.008	0.012 ^{NS}
	An	0.000	0.000	0.000	-0.001	-0.007	-0.001	0.009	-0.001	-0.053	0.028	0.014	0.001	0.005	0.003	0.197	0.193 ^{NS}
GNC	A	0.006	-0.002	-0.009	0.326	-0.087	-0.002	0.215	0.105	18.134	20.791	-38.712	-0.033	-0.633	-0.017	0.208	0.290 [*]
	An	0.000	0.000	0.000	0.010	-0.001	0.000	0.020	0.003	-0.112	-0.071	0.113	0.001	0.035	-0.006	0.383	0.374 ^{**}
SNC	A	0.013	-0.001	-0.004	0.522	-0.249	0.000	0.085	0.265	8.503	52.836	-61.181	0.265	-0.985	-0.026	0.108	0.151 ^{NS}
	An	0.000	0.000	0.000	-0.007	-0.001	0.000	0.005	0.012	0.015	-0.011	-0.002	0.000	-0.001	-0.005	-0.235	-0.231 [*]
GNV	A	-0.002	-0.004	-0.015	0.291	0.348	-0.001	0.118	0.068	32.955	2.227	-34.876	-0.280	-0.570	0.007	0.687	0.956 ^{**}
	An	0.000	0.000	0.000	0.020	-0.004	0.000	0.015	-0.001	-0.153	-0.108	0.161	0.001	0.050	-0.001	0.925	0.905 ^{**}
SNV	A	0.021	0.001	-0.010	1.023	-0.610	-0.001	0.059	0.185	0.968	75.804	-76.644	0.475	-1.247	-0.037	-0.033	-0.046 ^{NS}
	An	0.000	0.000	0.000	0.025	0.010	0.000	0.008	0.001	-0.093	-0.178	0.169	0.000	0.053	-0.010	0.602	0.588 ^{**}
BNV	A	0.019	-0.001	-0.015	1.044	-0.418	-0.001	0.100	0.195	13.797	69.744	-83.304	0.322	-1.356	-0.031	0.239	0.333 ^{**}
	An	0.000	0.000	0.000	0.025	0.005	0.000	0.012	0.000	-0.134	-0.164	0.185	0.000	0.058	-0.006	0.833	0.815 ^{**}
NHI	A	-0.019	-0.003	0.000	-0.737	0.749	0.001	0.012	-0.121	15.932	-62.154	46.269	-0.579	0.759	0.039	0.377	0.524 ^{**}
	An	0.000	0.000	0.000	-0.001	-0.015	0.000	0.010	-0.001	-0.092	0.045	0.027	0.001	0.008	0.008	0.505	0.494 ^{**}
NUPE	A	0.019	-0.001	-0.015	1.050	-0.425	-0.001	0.101	0.193	13.846	69.704	-83.315	0.324	-1.356	-0.032	0.239	0.333 ^{**}
	An	0.000	0.000	0.000	0.026	0.005	0.000	0.012	0.000	-0.133	-0.164	0.185	0.000	0.058	-0.007	0.828	0.809 ^{**}
NUtE	A	-0.020	-0.001	0.004	-0.823	0.723	0.002	-0.082	-0.154	4.957	-63.434	58.414	-0.508	0.961	0.044	0.209	0.291 [*]
	An	0.000	0.000	0.000	-0.010	-0.015	0.000	-0.009	-0.004	0.013	0.117	-0.082	0.001	-0.026	0.015	0.146	0.143 ^{NS}
NUE	A	-0.004	-0.004	-0.014	0.249	0.417	0.000	0.062	0.040	31.511	-3.493	-27.740	-0.304	-0.451	0.013	0.719	1.000 ^{**}
	An	0.000	0.000	0.000	0.022	-0.005	0.000	0.008	-0.003	-0.139	-0.105	0.151	0.001	0.047	0.002	1.022	1.000 ^{**}

Residual effect (R) -0.00006 and (I) -0.00000. E- Environment; A- Aerobic; An- Anaerobic. DF-Days to 50% flowering; PHMT-Plant height at maturity (cm); PL- Panicle length (cm); BY-Biological yield (g/m²); HI-Harvest index (%). CCFW- Chlorophyll content at flowering stage; GNC- Grain nitrogen content (%); SNC- Straw nitrogen content (%); GNV- Grain nitrogen yield (g/m²); SNV- Biomass nitrogen yield (g/m²); BNV- Biomass nitrogen yield (g/m²); NHI- Nitrogen harvest index (%); NUPE- Nitrogen uptake efficiency (gg-1N); NUtE- Nitrogen utilization efficiency (gg-1N) and NUE- Nitrogen use efficiency (gg-1N).

related traits. Moreover, Xu *et al.* (2016) concluded that in order to increase NUE, effective soil, plant, nutrient management measures, advances in knowledge and technologies would be required to sustain higher crop production.

4.5 Root traits study under different nitrogen regimes

Root system development is an important target for improving yield in cereal crops as it is one of the most important organs for plant growth due to the roles of water and mineral uptake. Active root systems that can take up nutrients more efficiently are essential for enhancing grain yield. The root morphological traits associated with the adaptation to N-depleted soils, the qualitative and quantitative importance of the root system in taking up N under N-limiting conditions has been pointed out in several studies (Guingo *et al.*, 1998; Kamara *et al.*, 2003; Coque and Gallais, 2006). It is difficult to evaluate the influence of the size, the volume, and the root system on NUpE and root traits related to yield from soil when plants are grown under agronomic conditions (Kondo *et al.*, 2003). To solve this problem, alternative techniques have been developed under controlled environmental conditions using either ‘rhizotrons’ (Devienne-Barret *et al.*, 2006 and Laperche *et al.*, 2006). Consequently, there are only a limited number of reports describing the response of the root morphology of cereals to different levels of N fertilization (Kondo *et al.*, 2003).

In order to analyze the morphological differences of the root of 12 selected cultivars. The genotypes were screened under zero nitrogen (N0), nitrate forms of nitrogen (NO_3^-) and ammonical form of nitrogen (NH_4^+) and their morphological characteristic including shoot length, root length, root diameter and root volume were measured using image analysis methods implemented in WinRHIZOPro system. Mean performance and genotypic differences of lines for root traits are presented in Table 4.12 and Fig. 4.1.

4.5.1 Mean performance of root traits under different forms of nitrogen

Analysis of means showed that, average shoot length under N^0 ranged from 17.48 to 42.55 mm with population mean of 34.35 cm. Whereas, under nitrate (NO_3^-) condition it ranges from 19.93 to 41.52 cm with a mean of 35.79 cm and under ammonium (NH_4^+) 26.23 to 48.82 cm with over all mean of 38.50 cm.

Root length under N^0 varied from 25.74 to 54.15 cm with mean of 40.82 cm. under NO_3^- condition it ranges from 14.90 to 38.35 cm with overall mean of 28.04 cm and under NH_4^+ condition root length ranged from 8.65 to 33.55 cm with average of 21.63 cm. Root diameter under N_0 condition ranged from 0.23 to 0.33 mm with mean of 0.27 mm, under NO_3^- condition ranged from 0.19 to 0.31 mm with mean of 0.25 mm and under NH_4^+ condition it ranges from 0.17 to 0.37 mm with average mean of 0.31 mm. The root volume under N_0 condition varied from 0.15 to 1.12 cm^3 overall mean of 0.61 cm^3 . Whereas under NO_3^- condition root volume ranged from 0.06 to 0.87 cm^3 with mean of 0.29 cm^3 and under NH_4^+ condition it ranged from 0.04 to 0.50 cm^3 with average mean of 0.23 cm^3 .

Under N^0 condition RCPR-8 had shown maximum shoot length 42.55 cm followed by RP-5125-2-4 (39.68 cm) and Samleshwari (39.27 cm) whereas minimum shoot length was reported by Indira Aerobic -1 (17.48 cm).

The genotype IR-64 (Drought) reported highest root length (54.15 cm) followed by RP-5125-2-4 (52.53 cm) and CR 3634-1-3 had shown lowest root length (25.74). The highest root diameter was reported by IR-64 (Drought) 0.33 mm followed by RCPR-8 and Digamber Dhan (0.31 mm) and lowest root diameter was reported by Indira Aerobic 1 (0.23 mm). IR-64 (Drought) had shown highest root volume of 1.12 cm^3 and CR-Dhan 3634-1-3 (0.15 cm^3) showed lowest root volume.

Under NO_3^- condition RCPR-8 had shown maximum shoot length 41.52 cm followed by Digamber Dhan (40.93 cm) and Samleshwari (40.20 cm) whereas minimum shoot length was reported by Indira Aerobic 1 (19.93 cm). The genotype Samleshwari reported highest root length (38.35 cm) followed by Digamber Dhan (38.02 cm) and IR-64 (Drought) (37.34 cm) whereas CR 3634-1-3 had shown lowest root length (14.90).

Table: 4.12 Genotypic differences for root and shoot traits among selected rice genotypes grown under mini-rhizotron (12 genotypes)

Sr. No.	Entry	N ⁰			NO ₃ ⁻			NH ₄ ⁺		
		Shoot length (cm)	Root length (cm)	Root diameter (mm)	Root volume (cm ³)	Shoot length (cm)	Root length (cm)	Root diameter (mm)	Root volume (cm ³)	Shoot length (cm)
1	Indira Aerobic 1	17.48	36.30	0.23	0.17	19.93	24.08	0.22	0.06	19.15
2	IR-64 Drought	36.28	54.15	0.33	1.12	34.73	37.34	0.25	0.53	32.45
3	Samleshwari	39.27	44.42	0.27	0.68	40.20	38.35	0.30	0.87	33.55
4	RP 5125-2-4	39.68	52.53	0.26	0.83	40.15	31.72	0.25	0.39	21.03
5	R 1882-306-4-243-1	29.75	42.95	0.28	0.60	31.33	24.57	0.25	0.11	25.63
6	RAU 1484-Aer-04	39.67	26.13	0.27	0.34	37.38	31.22	0.23	0.30	20.30
7	RCPR 8	42.55	50.97	0.31	0.94	41.52	17.28	0.31	0.21	16.25
8	CR 3631-1-3	33.05	31.60	0.28	0.54	38.18	22.98	0.27	0.23	14.99
9	CR 3632-1-2	36.38	50.32	0.26	0.72	35.68	19.63	0.23	0.13	20.30
10	CR 3634-1-3	28.32	25.74	0.24	0.15	29.57	14.90	0.19	0.06	8.65
11	Digamber Dhan	36.85	40.90	0.31	0.81	40.93	38.02	0.29	0.23	26.50
12	Dadhmaini Dhan	32.87	33.85	0.25	0.36	39.88	36.38	0.24	0.37	20.78
Mean		34.35	40.82	0.27	0.61	35.79	28.04	0.25	0.29	21.63
Min		17.48	25.74	0.23	0.15	19.93	14.90	0.19	0.06	8.65
Max		42.55	54.15	0.33	1.12	41.52	38.35	0.31	0.87	33.55
SE		1.96	2.92	0.01	0.09	1.81	2.46	0.01	0.07	2.04
SD		6.80	10.10	0.03	0.31	6.28	8.52	0.03	0.23	7.08

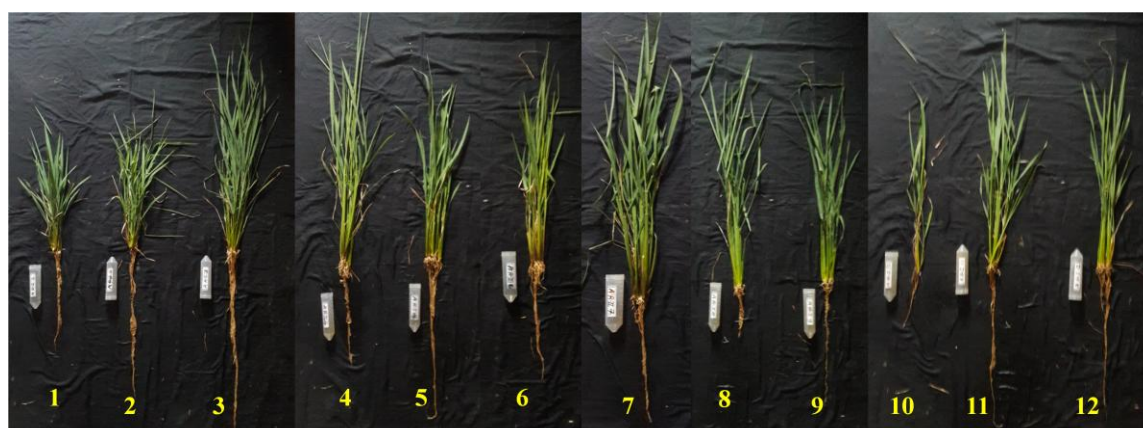
a) N^0N b) NO_3^-N c) NH_4^+N

Fig. 4.1 Variability and Morphological differences of root under N^0 , NO_3^- and NH_4^+ condition

The highest root diameter was reported by RCPR 8 (0.31 mm) followed by Samleshwari (0.30 mm) and Digamber Dhan (0.29 mm) and lowest root diameter was reported by CR 3634-1-3 (0.19 mm). Samleshwari had shown highest root volume of 0.87 cm^3 whereas lowest was reported by Indira Aerobic 1 (0.06 cm^3).

Under NH_4^+ condition CR 3631-1-3 had shown maximum shoot length 48.82 cm followed by Dadhmaini Dhan (45.05 cm) and R1882-306-4-243-1 (43.02 cm) whereas minimum shoot length was reported by CR 3634-1-3 (19.93 cm).

The genotype Samleshwari reported highest root length (33.55 cm) followed by IR-64 (Drought) (32.45 cm) whereas CR 3634-1-3 had shown lowest root length (14.90). The highest root diameters were reported by RP 5125-2-4, CR-3632-1-2 and Dadhmaini Dhan (0.37 mm) and CR 3634-1-3 (0.17 mm) showed lowest root diameter. Samleshwari had shown highest root volume of 0.50 cm^3 whereas lowest was reported by CR 3634-1-3 (0.04 cm^3).

In present study it is found that the shoot length was increases in NO_3^- and NH_4^+ compared to N^0 condition and but most of genotypes showed reduced root length in NH_4^+ and NO_3^- compared with N_0 condition this might be due the activity of root length increases as in N depleted soil, this study found no evidence on root length earlier by any worker. By contrast Thiem and Akira (2015) showed that increase of N level from 60 to 120 kg N ha^{-1} increased total root length and shoot dry weight of Nipponbare but did not increased those traits as increased N application from 120 to 180 kg N ha^{-1} . Although there are many several studies seems to be little information on differences in root morphology that may contribute to this variation. Root characteristics such as root length and root weight density have been identified as important factors because N uptake is determined by root mass and N uptake per unit root volume (Shimono and Bunce, 2009).

Among all genotypes under study, Samleshwari showed consistent performance under N^0 , NO_3^- and NH_4^+ conditions and IR-64 (Drought) also showed considerable performance over three conditions. The genotypes RP 5125-2-4, Dadhmaini Dhan, RAU 1482-306-4-243-1 and Digamber Dhan performed well in NO_3^- condition this might be due genotype shows desirable response in particular

form of N. Hamaoka *et al.* (2013) suggested that a high NUE is associated with the development of a root system, increased BR, and probably increased capacity of NO_3^- -N uptake.

4.5.2 Association of root traits on grain yield under different form of nitrogen

The character association and their direct and indirect on grain yield are presented in Table 4.13. In present study the character shoot length had shown positive but non-significant correlation with grain yield under N^0 ($r = 0.249$) and NH_4^+ ($r = 0.399$) and showed negative non-significant under NO_3^- . The root length showed positive but non-significant correlation with grain yield under N^0 condition and under NO_3^- and NH_4^+ root length showed negative but non-significant correlation with grain yield of $r = -0.240$ and $r = -0.059$ respectively. Root diameter recorded negative association with grain yield under N^0 condition whereas under NO_3^- and NH_4^+ it showed positive but non-significant correlation with grain yield. Root volume recorded negative association with grain yield under N^0 and NO_3^- condition but showed positive correlation under NH_4^+ . Such correlation is also reported by Gomez *et al.*, 2005; Mohankumar *et al.*, 2011 and Seyed Mostafa., 2013. This probably indicates that greater shoot length, root length and volume is of no specific advantage under NO_3^- condition where N is not a limiting factor and probably greater root length and volume require investment of carbon and other food assimilates for these plant parts, which adversely affect the grain yield.

Root volume exhibiting moderately positive direct effect on grain yield under N^0 condition whereas, under NO_3^- and NH_4^+ it exhibit low and high positive direct effect on grain yield respectively. Shoot length shown positive and moderate direct effect on grain yield under N^0 and NH_4^+ conditions. The character root length was showed positively moderate direct effect on grain yield under N^0 condition and under NO_3^- and NH_4^+ it showed negative direct effect on grain yield. Root diameter had exhibited high direct effect on grain yield under NO_3^- and NH_4^+ .

Table: 4.13 Correlation, direct and indirect effect of root traits over grain yield under three N regimes

Traits	E	Shoot length (cm)	Root length (cm)	Root diameter (mm)	Root volume (cm ³)	r value of grain yield
Shoot length (cm)	N ₀	0.543	0.085	-0.532	0.151	0.249
	NO ₃ ⁻	-0.288	-0.158	0.354	0.068	-0.023
	NH ₄ ⁺	0.301	-0.143	0.146	0.095	0.399
Root length (cm)	N ₀	0.223	0.209	-0.469	0.197	0.160
	NO ₃ ⁻	-0.112	-0.405	0.179	0.098	-0.240
	NH ₄ ⁺	0.096	-0.448	0.069	0.223	-0.059
Root diameter (mm)	N ₀	0.314	0.106	-0.921	0.191	-0.309
	NO ₃ ⁻	-0.190	-0.135	0.535	0.066	0.276
	NH ₄ ⁺	0.143	-0.101	0.306	0.112	0.462
Root volume (cm ³)	N ₀	0.362	0.181	-0.773	0.228	-0.002
	NO ₃ ⁻	-0.145	-0.294	0.262	0.135	-0.043
	NH ₄ ⁺	0.090	-0.314	0.108	0.318	0.202

Residual effects for N⁰: 0.547, NO₃⁻: 0.754 and NH₄⁺: 0.647.

In present study the character root volume exhibiting positive direct effect on grain yield under N⁰, NO₃⁻ and NH₄⁺ it indicate that the correlation between grain yield and this traits is due to direct effect of character, hence it reveals true relationship between them and direct selection for these traits will be rewarding for yield improvement. Whereas, root length exhibit negative direct effect on grain yield under NO₃⁻ and NH₄⁺ condition. The negative direct effect indicates that the direct selection through this trait would not prove to be useful for the improvement of grain yield under particular environment. The value of residual effect is moderate to high under three conditions; it indicates that beside the characters studied, there are some other traits which contribute for grain yield.

4.6 Stability analysis

Varietal adaptability to environmental fluctuation is important for the stabilization of crop production both over different environments and years. Adaptability is the ability or capability of a genotype to produce relatively narrow range of phenotype in different environments. Thus, stability proves the suitability of a variety for general cultivation over a wide range of environments.

The average performance of a genotype mainly depends on environmental interaction. Estimation of phenotype stability, which involves regression analysis, has proved to be valuable technique for assessing and reflecting the response of various genotypes under changing environmental conditions and genotype-environmental interactions given an idea of the buffering capacity of the population under study. Stability analysis includes location or environment wise analysis of variance and pooled analysis of variance for all environments or location.

If the G X E interaction is found significant the stability analysis can be worked out. In our study 38 genotypes were grown under three conditions i.e., zero nitrogen N0, Nitrogen in form of calcium nitrate (NO_3^-) and nitrogen in the form of ammonium chloride (NH_4^+) for both aerobic and anaerobic conditions. Using Eberhart and Russell model the data were analyzed separately for both aerobic and anaerobic condition to conclude the average performance of tested genotypes for grain yield over variables form of nitrogen and environments.

4.6.1 Analysis of variance for stability parameters

The analysis of variance for stability parameters was done according to the regression model of Eberhart and Russell (1966). The results of this study for grain yield are presented in Table 4.14. In aerobic condition variance due to genotype $\times$ environment was found non-significant indicating that linear response of genotypes to verifying environments i.e. genotypes tendered to adapt themselves with change in environments. Whereas in anaerobic condition genotype $\times$ environment was found significant indicating that differential response of genotypes to varying environmental condition and the analysis can be further done for estimating the stability parameters.

Similar Panwar *et al.* (2008) under pooled analysis of variance, of genotype x environment interaction. They reported significant genotype x environment interaction for grain yield. The significance of different effect was tested by variance ratio as per Eberhart and Russell (1966). The mean sum of square due to environment (linear) was significant when tested against pooled deviation with respect to grain yield, indicated differences between environments and their influence on genotypes for expressing of character.

Table: 4.14 Pooled analysis of variance and stability parameters for grain yield for different N regimes and variable environments during wet season 2016

Source of Variation	DF	Mean Squares	
		Aerobic	Anaerobic
Genotypes	37	6600.47**	19948.32**
Environments	2	40130.91**	20521.52**
Genotypes X Environments	74	317.63	3993.84**
Environments + (Genotypes X Environments)	76	1365.35**	4,428.78
Environments (Linear)	1	80261.82**	41043.05**
Environments X Genotypes (Linear)	37	418.37*	3,353.44
Pooled Deviation	38	211.19*	4512.28**
Pooled Error	111	256.24	720.81
Total	113		

Pooled Error MSS for testing pooled deviations for aerobic MSS 128.12 and for anaerobic 360.40

* and ** significant at 0.05 and 0.01 probability level, respectively.

Similarly Sawant *et al.* (2005) reported that the mean sum of square due to environment (linear) was significant when tested against pooled deviation with respect to grain yield, indicated differences between locations and their influence on genotypes for expressing of character. This is in accordance with previous reports on rice by Panwar *et al.*, 2008; Verma, 2013 and Vanave *et al.*, 2014. Akter *et al.* (2015) studied genotype × environment interaction and yield stability analysis in hybrid rice. Similar finding were also reported by Shantha *et al.*, 2007; Samrat *et al.*, 2010; Mosavi *et al.*, 2013 and Kota *et al.*, 2013.

4.6.2 Stability parameters for grain yield

Eberhart and Russell (1966) defined a stable variety as one with $b=1$ and $S^2di=0$. Using their definition a breeder would usually derive to develop a variety with

high mean and satisfying the values of b_i and S^2d_i . The mean performance and stability parameters for grain yield are given in Table 4.15. The overall mean grain yield pooled over three environments varied from 62.02 g/m² to 277.98 g/m² and 308.12 g/m² to 641.16 g/m² for aerobic and anaerobic condition respectively.

In anaerobic condition out of 38 genotypes, 20 genotypes showed higher mean grain yield than population mean. The genotypes RP-5125-2-4 had high value of mean grain yield with unit regression ($b_i=1$) and deviation was non-significant from zero (S^2d_i). This line gave stable performance under different form of nitrogen for both aerobic and anaerobic conditions. Koli and Chandra (2012) and Dewi *et al.* (2014) identified stable genotype based on regression coefficient.

In aerobic condition the genotype Samleshwari, RCPR-8, CR-3631-1-3, CR-3632-1-2 and in anaerobic condition the genotypes Indira Sona, RAU 1484-Aer-04, RCPR-8, CR 3631-1-3 and R-RF 105 had showed above average mean value for grain yield and $b_i>1$, indicating their suitability to favorable environment as they were highly sensitive to environmental condition. Hamam and Khaled (2009) suggest that days to heading, plant height, spike length, 1000-kernel weight, biomass and grain yield were significantly influenced by years, nitrogen fertilizer levels and genotypes and indicated that studied genotypes responded differently to the different environmental conditions suggesting the importance of the assessment of genotypes under different environments in order to identify the best genetic make up for a particular environment.

In aerobic condition high mean grain yield and regression $b_i<1$ were reported for genotypes Indira Sona, Digamber Dhan and Dadhmaini Dhan whereas in anaerobic condition, IR 84887-B-15, Indira Arobiec 1 and R 1672-1171-1-124-1. These lines were suitable for cultivation in unfavorable environment as there were least sensitive environmental changes.

Table: 4.15 Estimate of different stability parameters for grain yield for aerobic and anaerobic condition during wet season 2016

Genotypes	Aerobic			Anaerobic		
	Mean	(bi)	S ² di	Mean	(bi)	S ² di
Indira Sona	217.82	0.86	90.40	608.52	3.79	1867.42
Indira Aerobic 1	240.12	1.13	578.42	532.64	-0.39	-131.75
Swarna	62.02	0.64	-69.07	504.86	1.66	4472.59**
Basmati- 370	153.61	0.92	666.90	355.40	0.89	9839.43**
IR-64 Drought	265.30	1.13	-124.31	400.09	0.92	3220.51*
Samleshwari	251.44	1.57	-122.55	451.74	3.56	1634.21
Danteshwari	189.77	1.29	-6.44	308.12	1.39	4186.88*
RP 5125-2-4	277.98	1.02	-112.95	556.05	0.96	-315.77
R 1779-321-1-112-1	176.42	0.58	-120.21	515.00	-2.41	-261.04
R 1882-306-4-243-1	239.95	1.11	927.64*	570.34	-1.26	1486.25
R 2093-1536-1-660-1	170.84	0.30	162.67	463.36	-1.14	6155.25**
IR 84887-B-15	189.93	1.42	-127.47	614.21	0.59	1350.48
IR 83376-B-B-110-3	165.94	1.07	-65.72	559.23	0.69	14009.38**
R 1700-309-1-171-1	181.49	0.76	113.02	587.54	3.68	5787.48**
R 1672-1171-1-124-1	192.64	1.23	578.42	482.64	-0.79	1094.11
R 1262-1667-1-1	156.14	1.27	-41.80	428.11	0.59	6011.97**
R 1860-783-1-424-1	153.77	0.96	-31.22	507.05	-3.36	2987.10*
RAU 1484-Aer-04	234.88	0.96	-117.66	498.67	1.45	927.22
RCPR 8	245.53	1.59	-78.30	641.16	1.29	-256.13
CR 3631-1-3	249.25	1.83	-127.80	503.47	2.84	121.95
CR 3632-1-2	226.61	1.16	-124.68	480.22	2.82	9582.26**
CR 3634-1-3	177.94	0.66	-126.32	411.32	3.20	-360.04
CR Dhan 40	137.55	0.61	-96.25	373.33	0.83	-190.68
R-RHZ-2	151.58	1.08	311.70	370.51	2.80	1744.24
R-RF 105	149.04	1.73	165.68	482.14	2.05	-288.95
R 1670-3269-2-3926-1	190.44	1.77	143.04	501.91	0.92	9706.80**
R 1902-912-2-512-1	146.68	1.37	-81.10	425.38	0.64	14469.47**
MTU-1010	140.09	0.71	-126.79	450.87	0.13	-75.32
R 1570-2644-2-1547-1	188.42	1.84	42.63	517.94	-0.39	12897.02**
R 1432-251-103-1-1	147.18	0.12	-83.05	391.44	-2.88	2905.93*
CGR-547 (Bargi)	172.19	0.78	23.44	406.68	-0.35	191.43
Digamber Dhan	189.26	0.41	-92.85	358.50	2.33	12811.12**
Dadhmaini Dhan	188.58	0.89	-81.45	408.06	3.11	-244.87
CR Dhan 201	168.47	0.93	164.83	399.41	0.91	4280.94**
CR Dhan 202	159.18	0.18	911.10*	510.23	2.76	10685.18**
IR-64	172.70	0.92	-97.86	392.65	1.15	5612.32**
Indira Barani Dhan 1	149.04	0.41	344.20	467.90	0.75	10181.49**
Sampada	75.37	0.78	-11.54	356.11	2.26	-324.50

Grain yield in g/m² population mean for aerobic = 182.77 g/m² and for anaerobic 468.23 g/m²,

bi = regression, S²di = Deviation from regression

* and ** significant at 0.05 and 0.01 probability level, respectively.

4.7 Quality study

In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. But rice is the only cereal crop cooked and consumed mainly as whole grains and consumers are mainly concerned with post-cooking quality of rice. Hence, quality considerations are more important (Hossain *et al.*, 2009). The present study aimed to assess the nature and magnitude of genetic diversity, variability, correlation of 12 quality traits of 38 rice genotypes in order to select suitable highly diverse genotypes as parents for further utilization in grain quality improvement programs through heterotic breeding and for subsequent progeny selection through pedigree method.

4.7.1 Mean phenotypic performance of quality traits over aerobic and anaerobic condition

The mean, range, standard error and standard deviation of 12 quality traits for 38 selected rice germplasm accessions under aerobic and anaerobic condition is presented in Appendices-J and K respectively.

1. Hulling percent (%)

In aerobic condition hulling percentage ranged from 68.70% to 80.10% with an overall mean performance of 75.83%. The maximum hulling percent was recorded in R 1672-1171-1-124-1 (80.10%), followed by R 1262-1667-1-1 (79.72%) and RP 5125-2-4 (79.38%). In anaerobic condition, hulling percentage ranged from 67.22% to 79.22 with mean value 74.59%. The genotypes IR 83376-B-B-110-3 and CR 3631-1-3 had shown maximum hulling percent (79.22), followed by Swarna (78.50%) and R 1432-251-103-1-1 (78.10%). The minimum hulling percent was recorded in Indira Barani Dhan-1 (68.70%) and (67.22) under both conditions.

2. Milling percent (%)

In aerobic condition milling percentage ranged from 54.90% to 72.98% with an overall mean performance of 65.04%. The maximum milling percent was recorded in RP 5125-2-4 (72.98%) and R 1262-1667-1-1 (71.00%). Genotype R 1882-306-4-

243-1 had shown minimum milling percent (54.90). In anaerobic condition milling percentage ranged from 50.58 to 69.78 percent with an overall mean performance of 61.79 percent. The maximum milling percent were recorded in R 1570-2644-2-1547-1 (69.78%), Swarna (68.24%) and RAU 1484-Aer-04 (68.00%) while CGR-547 (Bargi) had shown minimum milling percent (50.58).

3. Head Rice Recovery (%)

The head rice recovery was found in the ranged from 21.52 to 57.20 percent with an overall average of 37.50% and 33.12 to 56.38 with overall mean 46.37 % under aerobic and anaerobic conditions, respectively. In aerobic condition highest head rice recovery was recorded in R 1860-783-1-424-1 (57.20%) followed by RAU 1484-Aer-04 (46.62%) and IR 84887-B-15 (46.48%). Whereas, in anaerobic condition R 1570-2644-2-1547-1 (56.38%), R 1700-309-1-171-1 (55.98%) and Dadhmaini Dhan (55.28%) reported maximum head rice recovery percent. The genotype Indira Sona (21.52%) and R –RF 105 (33.12%) had shown minimum head rice recovery under aerobic and anaerobic conditions respectively.

4. Kernel length (mm)

In aerobic field kernel length of milled grain ranged from 4.80 to 6.80 mm with an overall mean of 5.72 mm. The maximum milled kernel length was recorded in Indira Sona (6.80 mm) and CR 3634-1-3 (6.60 mm). Indira Aerobic 1 (4.80) recorded minimum kernel length. In anaerobic condition kernel length of milled grain ranged from 5.20 to 7.00 mm with an overall mean of 5.79 mm. The maximum milled kernel length was recorded in Indira Sona (7.00 mm) followed by R 2093-1536-1-660-1 and CR 3632-1-2 (6.40 mm). The genotypes Indira Aerobic 1, Swarna, R 1570-2644-2-1547-1, Digamber Dhan and Dadhmaini Dhan (5.20) recorded minimum kernel length.

5. Kernel breadth (mm)

The kernel breadth of milled grain for aerobic condition ranged from 1.80 mm to 2.80 mm with an overall mean of 2.24 mm and for anaerobic condition it ranged

from 2.00 mm to 2.60 mm with overall mean of 2.18 mm. R 1262-1667-1-1 (2.80) and RCPR 8 (2.60) depicted maximum kernel breadth under aerobic and anaerobic conditions respectively. The lowest breadth of milled grain was recorded in Basmati-370 (1.80 mm) and (2.00 mm) in aerobic and anaerobic conditions respectively.

6. L/B ratio before

In aerobic condition L/B ratio of milled grain ranges from 1.86 to 3.33 with an average performance of 2.59. The maximum L/B ratio of milled grain was recorded in CR 3634-1-3 and Basmati 370 (3.3) followed by Indira Sona, R 1700-309-1-171-1 and CR Dhan 201 (3.1). The minimum L/B ratio of milled grain was recorded in R 1262-1667-1-1 (1.86). In anaerobic condition L/B ratio of milled grain ranged from 2.15 to 3.50 with an average performance of 2.67. The maximum L/B ratio of milled grain was recorded in Indira Sona (3.5) followed by Basmati 370 and Danteshwari (3.1). The minimum L/B ratio of milled grain was recorded in RCPR 8 (2.15).

7. Kernel length after cooking (mm)

The kernel length after cooking for aerobic condition ranged from 6.80 mm to 9.60 mm with an overall average 8.50 mm. The maximum length of cooked kernel was recorded in Samleshwari (9.6 mm) followed by R 1672-1171-1-1-124-1, R 1670-3269-2-3926-1 (9.4 mm) and CR Dhan 201 (9.2 mm). The minimum length of cooked kernel was recorded in CR Dhan 40 (6.80 mm). In anaerobic condition kernel length after cooking in genotypes ranged from 7.00 mm to 9.80 mm with an overall average 8.76 mm. The maximum length of cooked kernel was recorded in Samleshwari and R 1670-3269-2-3926-1 (9.8 mm) followed by RP 5125-2-4 (9.6 mm) and R 1779-321-1-112-1 (9.4 mm). The minimum length of cooked kernel was recorded in CR Dhan 40 (7.0 mm).

8. Kernel breadth after cooking (mm)

In aerobic condition the kernel breadth after cooking ranged from 2.20 mm to 3.00 mm with an average of 2.67 mm. The maximum breadth of cooked kernel was recorded in R 1672-1171-1-124-1, R 1262-1667-1-1 and CGR-547 (Bargi) (3 mm)

and the minimum breadth of cooked kernel was recorded in R 1432-251-103-1-1 (2.20 mm). Whereas for anaerobic condition kernel breadth after cooking ranged from 2.60 to 3.60 mm with overall mean of 3.04. Genotype CGR-547 (Bargi) reported highest kernel breadth (3.6 mm), followed by R 2093-1536-1-660-1 and Swarna (3.40 mm). The minimum kernel breadth was recorded in R 1432-251-103-1-1 (2.60 mm)

9. L/B ratio of after cooking

The L/B ratio of cooked kernel ranged from 2.43 to 3.91 with an average of 3.21 and from 2.33 to 3.50 with an average 2.90 for aerobic and anaerobic condition respectively. R 1432-251-103-1-1 (3.91) reported maximum L/B ratio of cooked kernel for aerobic condition and Samleshwari (3.50) reported maximum L/B ratio of cooked kernel for anaerobic condition. The minimum L/B ratio of cooked kernel was recorded in CR Dhan 40 (2.40) and (2.30) for both conditions respectively.

10. Elongation ratio

The variation in elongation ratio for aerobic ranged from 1.21 to 1.85 with the overall mean of 1.49. The highest elongation ratio was recorded in Samleshwari (1.85) followed by Indira Aerobic 1 (1.75) and R 1672-1171-1-124-1 (1.74). The minimum elongation ratio was recorded in CR Dhan 40 (1.21). In case of anaerobic condition, elongation ratio ranged from 1.30 to 1.74 with the overall mean of 1.52. The highest elongation ratio was recorded in R 1672-1171-1-124-1 (1.74) followed by Dadhmaini Dhan (1.73). The minimum elongation ratio was recorded in IR 83376-B-B-110-3 and CR Dhan 40 (1.30).

11. Elongation index

In aerobic condition elongation index ranged from 0.95 to 1.70 with an overall mean of 1.26. The highest elongation index was recorded in Samleshwari (1.70) followed by R 1262-1667-1-1 (1.58) and Indira Aerobic 1 (1.50). The lowest elongation index was recorded in CR Dhan 40 (0.95). Whereas, in anaerobic condition elongation index ranged from 0.85 to 1.43 with an overall mean of 1.10. The highest

elongation index was recorded in R 1262-1667-1-1 (1.43) and RAU 1484-Aer-04 (1.38). The lowest elongation index was recorded in R 2093-1536-1-660-1 (0.85).

12. Water uptake (ml)

The water uptake for aerobic condition ranged from 135.00 ml to 340.00 ml with an overall mean of 241.84 ml and for anaerobic condition it ranged from 110.00 ml to 320.00 ml with overall mean of 235.39 ml. The maximum water uptake was reported in Dadhmaini Dhan (340 ml and 320.00 ml) under both conditions respectively, followed by R 1700-309-1-171-1, Digamber Dhan and Indira Barani Dhan 1 (335 ml and 310 ml each). The lowest water uptake was recorded in CR 3631-1-3 of 135 ml and 110.00 ml under aerobic and anaerobic conditions respectively.

The genetic variability in any breeding material is a prerequisite as it does not only provide a basis for selection and some valuable information regarding selection of diverse parents for use in hybridization programme. Similar finding for quality traits were also reported by Sarkar *et al.* (2007), Singh and Singh (2007), Bajpai and Singh (2010), Shilpa *et al.* (2010) and Danbaba *et al.* (2011).

Parikh *et al.* (2012) and Sarawgi *et al.* (2012) suggested that genotypes having good quality grain may be used in hybridization programme to achieve desired segregants for good grain quality with higher yield. Subudhi *et al.* (2012), Kumari *et al.* (2013), Pachauri *et al.* (2013), Vanisree *et al.* (2013) and Hosen *et al.* (2016) also revealed significant differences among genotypes for yield, its components and grain quality traits. Gangadharaiah *et al.* (2015) studied the physicochemical and cooking quality of traditional rice cultivars grown in the farmer's field. Among the cultivars, Kichadi Sona and Salem Sanna recorded higher milling yield (66.0% and 65.0%) and head rice recovery (58.5% and 58.30%), respectively. Therefore, these cultivars could be utilized in the breeding programme is the need of the today towards the "hidden hunger" free world.

4.7.2 Correlation study

Correlation estimates showed the possibility of improvement of a character through selection for other character. The correlation coefficient analysis is the index of association between two variables. These have been dealt in all possible combination for important of characters and are presented in Table 4.16. The character hulling percent showed significant and positive correlation with milling percent ($r = 0.435$) and ($r = 0.343$) under both aerobic and anaerobic conditions respectively. The milling percent also showed positive and significant association with head rice recovery ($r = 0.454$ and $r = 0.628$) under both conditions. In aerobic condition head rice recovery showed negative but non-significant correlations with kernel length ($r = -0.294$) and L/B ratio ($r = -0.212$) whereas, in anaerobic condition head rice recovery had shown negative but significant correlation with kernel length ($r = -0.427$) and L/B ratio ($r = -0.380$).

In both conditions kernel length showed negative but significant correlation with kernel breadth ($r = -0.327$ and $r = -0.425$), elongation ratio ($r = -0.712$ and $r = -0.573$) and elongation index ($r = -0.576$ and $r = -0.504$) but showed positive and significant correlation with L/B ratio ($r = 0.791$ and $r = 0.845$). In aerobic condition kernel length after cooking had shown positive but non-significant correlation with kernel length after cooking ($r = 0.298$) and significant ($r = 0.353$) in anaerobic condition. This trait also showed positive correlation with L/B ratio after cooking in both conditions.

The kernel breadth showed negative but significant correlation with L/B ratio ($r = -0.828$ and $r = -0.839$) in both aerobic and anaerobic conditions respectively. Whereas this trait showed positive and significant association with elongation ratio ($r = 0.335$ and $r = 0.330$) and elongation index ($r = 0.585$ and $r = 0.642$). The trait L/B ratio showed positive correlation with L/B ratio after cooking ($r = 0.425$ and $r = 0.256$) but showed negative and significant correlation with elongation ratio ($r = -0.616$ and $r = -0.539$) and elongation index ($r = -0.711$ and $r = -0.675$) under both aerobic and anaerobic conditions respectively.

In both aerobic and anaerobic conditions, the trait kernel length after cooking was found positive and significantly correlated with L/B ratio after cooking ($r = 0.691$ and $r = 0.736$), elongation ratio ($r = 0.453$ and $r = 0.561$) and elongation index ($r = 0.396$ and $r = 0.352$). Whereas kernel breadth after cooking showed negative but significant correlation with L/B ratio after cooking ($r = -0.804$ and $r = -0.761$) in aerobic and anaerobic condition respectively. L/B ratio after cooking in anaerobic condition had shown positive and significant correlation with elongation ratio ($r = 0.387$) and elongation index ($r = 0.534$) but in case of aerobic condition these two trait showed positive but non-significant association among them. Elongation ratio was reported positively significant correlation with elongation index ($r = 0.832$ and $r = 0.752$) for both conditions.

In case of water uptake, this trait was not shown any association among other quality traits in aerobic condition but in anaerobic condition water uptake showed negative and significant association with kernel breadth ($r = -0.387$) and elongation index ($r = -0.335$).

In the present study the positive significant correlation of hulling % with milling % and head rice recovery indicated that the genotypes with higher hulling percent also showed higher estimates for milled rice and head rice. Head rice recovery had significant and positive correlation with milling percent is in confirmation with the findings of Ekka *et al.* (2011) and Devi *et al.* (2015b). Their study also suggest that hulling %, milling % and HRR % are important quality attributes for rice that enhances commercial success of a variety. Simultaneous improvement of these 3 quality traits namely hulling percent, milling percent and head rice recovery can be made with the selection of a single trait is either hulling percent or milling percent or head rice recovery.

In this study, kernel length after cooking and kernel elongation ratio are interdependent as evidenced by the positive significant association between them. Hence, selection of either of the trait will ultimately enhance the mean performance of the interdependent trait (Devi *et al.*, 2015b).

Table: 4.16 Correlation of 12 quality traits of 38 selected rice accession under aerobic and anaerobic condition

Traits	E	H (%)	M (%)	HRR (%)	KL (mm)	KB (mm)	L:B	KLAC (mm)	KBAC (mm)	L:B(AC)	ER	EI	WU (ml)
H (%)	A	1.00	0.435**	0.117	-0.023	0.266	-0.176	0.271	-0.030	0.177	0.213	0.331*	-0.035
	An	1.00	0.343*	0.214	-0.096	0.036	-0.059	-0.125	-0.150	0.041	-0.011	0.090	-0.250
M (%)	A		1.00	0.454**	-0.310	0.242	-0.337*	-0.074	0.154	-0.162	0.223	0.232	-0.046
	An		1.00	0.628**	-0.119	0.024	-0.080	-0.150	-0.248	0.057	-0.027	0.136	-0.064
HRR (%)	A			1.00	-0.294	0.061	-0.212	-0.081	-0.089	0.010	0.194	0.225	-0.287
	An			1.00	-0.427**	0.220	-0.380*	-0.033	-0.196	0.098	0.349*	0.424**	-0.159
KL (mm)	A				1.00	-0.327*	0.791**	0.298	-0.234	0.331*	-0.712**	-0.576**	0.027
	An				1.00	-0.425**	0.845**	0.353*	-0.081	0.287	-0.573**	-0.504**	0.124
KB (mm)	A					1.00	-0.828**	0.035	0.545**	-0.371*	0.335*	0.585**	-0.125
	An					1.00	-0.839**	-0.050	0.168	-0.140	0.330*	0.642**	-0.387*
L:B	A						1.00	0.169	-0.461**	0.425**	-0.616**	-0.711**	0.073
	An						1.00	0.234	-0.154	0.256	-0.539**	-0.675**	0.307
KLAC (mm)	A							1.00	-0.132	0.691**	0.453**	0.396*	-0.182
	An							1.00	-0.128	0.736**	0.561**	0.352*	-0.060
KBAC (mm)	A								1.00	-0.804**	0.122	-0.098	-0.192
	An								1.00	-0.761**	-0.035	-0.443**	0.051
L:B(AC)	A									1.00	0.195	0.320	0.045
	An									1.00	0.387*	0.534**	-0.071
ER	A										1.00	0.832**	-0.162
	An										1.00	0.752**	-0.157
EI	A											1.00	-0.083
	An											1.00	-0.335*
WU (ml)	A												1.00
	An												1.00

* and ** significance at .05 and .01 levels respectively. E- Environment; A- Aerobic; An-Anaerobic. H- Hulling percent; M-Milling percent; HRR-Head Rice Recovery percent; KL-Kernel length; KB-Kernel breadth; L:B-Kernel length: Breadth ratio; GS- Grain shape; KLAC-Kernel length after cooking; KBAC-Kernel breadth after cooking; L:B (AC)-Length: Breadth ratio after cooking; ER-Elongation ratio; EI-Elongation index; WU-Water uptake.

The kernel breadth showed highly significant but negative correlation with L/B ratio similar association was earlier reported by Khatun *et al.* (2003). Similarly Allam *et al.* (2015) reported that Kernel L/B ratio showed positive and significant correlation with KLAC ($r_p=0.5510$, $r_g=0.5790$) and showed negative and significant correlation with elongation ratio ($r_p = -0.4235$, $r_g = -0.4397$).

The study suggested that kernel length, kernel L/B ratio, KLAC and elongation ratio are important traits which should be used as selection criteria to develop high yielding and better quality varieties.

L/B ratio is a good indicator of kernel length after cooking. Thus higher the L/B ratio, more the kernel length after cooking. Selection for these significantly and positively correlated traits will improve the overall quality trait (Devi *et al.*, 2015b). Kernel length and Kernel breadth respectively had positive and negative correlations with length breadth ratio similar finding was also reported by Gnanasekaran *et al.* (2008) and Makwana *et al.* (2010).

4.7.3 Cluster analysis

Cluster analysis among 38 rice germplasm accessions/genotypes was studied for 12 quality traits. These 38 entries were grouped into 8 clusters and clustering pattern of all the genotypes for both aerobic and anaerobic conditions are presented in Tables 4.17.1 and 4.17.2.

In aerobic condition the highest number of genotypes appeared in Cluster I, which contain 8 genotypes followed by Cluster II (7 accessions), Cluster V (6 accessions), Cluster VI (5 accessions), III and VIII (4 accessions), Cluster IV and VII (2 accession). Whereas in anaerobic condition the highest number of genotypes appeared in Cluster I and II, which contain 7 genotypes followed by Cluster III (6 accessions), Cluster VI (5 accessions), Cluster IV, V and VII (4 accessions) and VIII (1 accessions). The pattern of group constellation proved the existence of significant amount of variability.

Table: 4.17.1 Clustering pattern of 38 rice genotypes based on D² analysis for aerobic condition

Cluster No.	Number of genotypes	Name of genotypes
I	8	Indira Sona, IR-64 Drought, R 1779-321-1-112-1, IR 83376-B-B-110-3 RAU 1484-Aer-04, R-RF 105, CR Dhan 202, IR-64
II	7	Indira Aerobic 1, Samleshwari, R 2093-1536-1-660-1, R 1672-1171-1-124-1 CR 3631-1-3, R-RHZ-2, R 1570-2644-2-1547-1
III	4	Swarna, R 1860-783-1-424-1, CR 3632-1-2, CGR-547 (Bargi)
IV	2	Basmati- 370, MTU-1010
V	6	Danteshwari, IR 84887-B-15, RCPR 8, CR 3634-1-3 R 1902-912-2-512-1, Sampada
VI	5	RP 5125-2-4, R 1262-1667-1-1, CR Dhan 40, R 1670-3269-2-3926-1 CR Dhan 201
VII	2	R 1882-306-4-243-1, R 1432-251-103-1-1
VIII	4	R 1700-309-1-171-1, Digamber Dhan, Dadhmaini Dhan, Indira Barani Dhan 1

Table: 4.17.2 Clustering pattern of 38 rice genotypes based on D² analysis for anaerobic condition

Cluster No.	Number of genotypes	Name of genotypes
I	7	RP 5125-2-4, RAU 1484-Aer-04, CR 3632-1-2, CR 3634-1-3, MTU-1010, Swarna, Danteshwari
II	7	R 1779-321-1-112-1, R 1860-783-1-424-1, R-RF 105, R 1670-3269-2-3926-1 CGR-547 (Bargi), IR-64 Drought, CR Dhan 202
III	6	R 1882-306-4-243-1, IR 83376-B-B-110-3, R 1432-251-103-1-1, Indira Sona, CR Dhan 201, IR-64
IV	4	R 2093-1536-1-660-1, IR 84887-B-15, R 1672-1171-1-124-1, Samleshwari
V	4	R 1700-309-1-171-1, Digamber Dhan, Dadhmaini Dhan, Indira Barani Dhan 1
VI	5	R 1262-1667-1-1, CR Dhan 40, R 1902-912-2-512-1, Basmati- 370, Sampada
VII	4	RCPR 8, R-RHZ-2, R 1570-2644-2-1547-1, Indira Aerobic 1
VIII	1	CR 3631-1-3

The inter and intra cluster distances among eight clusters under aerobic and anaerobic conditions were computed and are given in Table 4.18. In aerobic condition the intra cluster D² values ranged from 5.50 (cluster VII) to 10.03 (cluster III) followed by cluster II (9.12), cluster VIII (7.91), cluster V (7.55), cluster I (6.40), cluster VI (6.07) and cluster IV (5.99). In anaerobic condition the intra cluster D² values ranged from zero (cluster VIII) to 9.40 (cluster III) followed by cluster I (8.52),

cluster II (8.49), cluster V (6.60), cluster VII (6.27), cluster VI (5.57) and cluster IV (5.43).

Table: 4.18 Average intra (diagonal) and inter cluster distances for quality traits

Aerobic								
Cluster	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster	VIII cluster
I cluster	6.40	128.82	26.88	100.09	75.38	49.78	25.52	51.50
II cluster		9.12	103.60	28.98	53.60	79.73	153.82	179.87
III cluster			10.03	75.25	50.07	24.94	50.90	76.54
IV cluster				5.99	25.30	51.57	125.07	151.32
V cluster					7.55	26.81	100.27	126.34
VI cluster						6.07	74.92	100.36
VII cluster							5.50	27.45
VIII cluster								7.91
Anaerobic								
Cluster	I cluster	II cluster	III cluster	IV cluster	V cluster	VI cluster	VII cluster	VIII cluster
I cluster	8.52	54.49	85.45	23.63	105.58	27.99	47.35	97.62
II cluster		8.49	31.21	77.83	52.24	26.59	101.82	152.08
III cluster			9.40	108.89	22.78	57.60	132.72	182.94
IV cluster				5.43	128.94	51.30	24.54	74.52
V cluster					6.60	77.97	152.59	202.62
VI cluster						5.57	75.28	125.53
VII cluster							6.27	50.30
VIII cluster								0.00

The maximum inter cluster distance was reported between cluster II and cluster VIII (179.87) in aerobic condition and between clusters V and VIII (202.62) in anaerobic condition; indicating that selection of genotypes belongs to distant clusters were expected to execute maximum heterosis upon crossing and can used in hybridization program for obtaining a wide spectrum of variation among the segregants. The least inter cluster distance was observed between cluster III and VI (24.94) for aerobic and between cluster III and V (22.78) for anaerobic condition this indicates genotypes of these clusters were closely related.

The highest intra cluster distance was reported in cluster III (10.03) and (9.40) for aerobic and anaerobic condition respectively, this indicates wide genetic variation among the genotypes belonging to this cluster. Cluster VIII had only one genotype hence zero intra cluster distance was reported in anaerobic condition.

The cluster mean values of twelve qualitative characters for both conditions were presented in Table 4.19. This was helpful to assess the superiority of clusters.

In aerobic condition the sixth group of cluster had the highest cluster mean value for traits viz., milling (70.06), kernel length (6.20), L/B ratio (3.10) and kernel length after cooking (9.20). Cluster I had the highest cluster mean for kernel breadth (2.40) and elongation index (1.47). Cluster III and IV had highest cluster mean value for trait head rice recovery (44.80) and hulling percent (78.40) respectively. Cluster VII had highest cluster mean value for L/B ratio after cooking (3.91) and VIII for elongation ratio (1.72).

In case anaerobic condition the fifth group of cluster had the highest cluster mean value for traits viz., milling (64.80), head rice recovery (54.84), elongation ratio (1.58) and water uptake (310).

Cluster I, II and III had the highest cluster mean for kernel length, L/B ratio, L/B ratio after cooking and elongation ratio and cluster VII reported highest cluster mean for trait kernel breadth and kernel breadth after cooking.

Similar finding were also reported by Devi *et al.* (2015a) and Ravindra Babu *et al.* (2006). Subudhi *et al.* (2009) also evaluated physico-chemical and cooking characters in rice to study the diversity pattern among the genotypes and reported that the characters kernel length after cooking and kernel breadth together accounted for genetic divergence. Roy *et al.* (2007) also reported that cooked kernel length contributed the maximum towards genetic divergence.

The selection and choice of parents mainly depends upon contribution of characters towards divergence. It is well known that crosses between divergent parents usually produce greater heterotic effect than between closely related ones Hossain *et al.* (2003).

Table: 4.19 Cluster mean values for different quality traits under aerobic and anaerobic condition

Cluster	E	H (%)	M (%)	HRR (%)	KL (mm)	KB (mm)	L:B (mm)	KLAC (mm)	KBAC (mm)	L:B (AC)	ER	EI	WU (ml)
I	A	76.80	64.30	33.14	5.40	2.40	2.25	8.60	2.60	3.31	1.59	1.47	285.00
	An	76.40	58.80	42.48	6.00	2.00	3.00	8.80	2.80	3.14	1.47	1.05	210.00
II	A	75.60	64.70	39.74	5.90	2.40	2.46	8.00	2.60	3.08	1.36	1.25	160.00
	An	72.94	60.68	39.38	6.00	2.00	3.00	9.40	3.10	3.03	1.57	1.01	260.00
III	A	74.50	64.80	44.80	5.20	2.40	2.20	7.60	3.00	2.50	1.46	1.17	260.00
	An	75.26	63.28	44.08	6.00	2.00	3.00	9.40	3.20	2.94	1.57	0.98	295.00
IV	A	78.40	68.00	34.70	6.00	2.00	3.00	8.20	2.60	3.15	1.37	1.05	185.00
	An	75.60	59.30	49.00	5.60	2.40	2.33	8.60	2.80	3.07	1.54	1.32	185.00
V	A	77.16	60.10	35.46	6.00	2.00	3.00	8.60	2.40	3.58	1.43	1.19	210.00
	An	73.20	64.80	54.84	5.20	2.20	2.36	8.20	3.20	2.56	1.58	1.08	310.00
VI	A	75.56	70.06	35.38	6.20	2.00	3.10	9.20	2.80	3.29	1.48	1.06	235.00
	An	73.26	60.24	46.16	5.40	2.20	2.45	8.20	3.00	2.73	1.52	1.11	235.00
VII	A	73.74	63.64	37.08	5.80	2.00	2.90	8.60	2.20	3.91	1.48	1.35	310.00
	An	77.30	63.60	53.40	5.60	2.60	2.15	8.60	3.20	2.69	1.54	1.25	160.00
VIII	A	76.20	67.44	32.64	5.00	2.20	2.27	8.60	2.60	3.31	1.72	1.46	340.00
	An	79.22	65.08	54.56	6.00	2.40	2.50	8.80	3.00	2.93	1.47	1.17	110.00

E- Environment; **A-** Aerobic; **An-** Anaerobic; **H-** Hulling percent; **M-** Milling percent; **HRR-** Head Rice Recovery percent; **KL-** Kernel length; **KBBC-** Kernel breadth; **L:B-** Length:Breadth ratio; **GS-** Grain shape; **KLAC-** Kernel length after cooking; **KBAC-** Kernel breadth after cooking; **L:B (AC)-** Length:Breadth ratio after cooking; **ER-** Elongation ratio; **EI-** elongation index; **WU-** Water uptake.

Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that parental lines selected from cluster VI, V and VIII for hulling, milling, head rice recovery per cent, kernel length, L/B ratio, kernel length after cooking and elongation index would be used in crossing programmes to achieve desired segregants.

The genotypic distribution also indicated that the genotypes originated from similar geographic regions were distributed in different clusters. That might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions. Similar findings of non correspondence of genetic divergence with geographic diversity were reported earlier in rice by Murthy and Arunachalam (1966), Rajesh *et al.* (2010) and Devi *et al.* (2015a). Considering this parents should be selected on the basis of genetic diversity rather than geographic diversity which are supported by the findings of Hassan *et al.* (2000). Grouping of materials of similar origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin. So genotypes originating from same place may have different genetic architecture or *vice versa* (Shanmugam and Rangaswamy, 1982).

Ramaiah (1969) classification is used to assign the grain shape based on length and length /breadth ratio. In aerobic condition 20 genotypes classified as short bold, 9 as a medium slender and 4 as a long slender and long bold. In anaerobic condition eighteen genotypes out of 38, classified as medium slender followed by short bold (15 genotypes), long bold and long slender has two genotypes each. The genotype Indira Sona reported Basmati type of grain in both conditions.

4.7.4 Iron and Zinc content

Rice with significant mineral content would be great advantages to half of the world population. Identification of mineral enhancing genotype in rice could help to further increase the content of iron/zinc or both in grain. In present study, Iron and zinc content were estimated by using energy dispersive X-ray fluorescent spectrophotometer (ED-XRF) for 38 rice accession under different nitrogen regimes

for aerobic and anaerobic conditions. The comparative genotypic differences are presented in Appendix-L. Mean, ranges and top ranked genotype of Zn content are presented in Tables 4.20.1, 4.20.2 and 4.20.3.

In aerobic condition Fe ranged from 6.9 to 12.3 ppm in zero nitrogen (N^0), 6.7 to 16.2 ppm in nitrate form of nitrogen (NO_3^-) and 7.1 to 20.8 ppm in ammonium forms of nitrogen (NH_4^+). The overall mean value of Fe was 9.1, 10.4, and 11.3 ppm under N^0 , NO_3^- and NH_4^+ respectively. Whereas zinc content in brown rice was varied from 6.7 to 20.6 ppm, 6.3 to 21.4 ppm and 6.7 to 24.9 ppm with overall mean of 14.1, 11.9, and 16.1 ppm under N^0 , NO_3^- and NH_4^+ respectively.

In anaerobic condition Fe ranged from 7.6 to 12.8 ppm, 7.8 to 13.2 ppm and 8.9 to 13.7 ppm with overall mean of 9.6, 10.2, and 10.9 ppm for N^0 , NO_3^- and NH_4^+ respectively. Zn content was ranged from 14.0 to 25.6 ppm with an average of 19.5 ppm for zero nitrogen. In NO_3^- and NH_4^+ Zn content ranges from 14.7 ppm to 25.5 ppm and 14.8 ppm to 25.7 ppm respectively with overall mean of 19.4 ppm in NO_3^- and 20.5 ppm in NH_4^+ . Estimation of Fe and Zn of 38 rice genotypes grown under N^0 , NO_3^- and NH_4^+ forms of nitrogen revealed that the average Fe of these genotypes (brown rice) in aerobic condition increased from 9.1 ppm under N^0 to 10.4 ppm and 11.3 ppm under NO_3^- and NH_4^+ respectively.

The Zn increased from 14.1 ppm under N^0 to 16.1 ppm under NH_4^+ form of nitrogen. In anaerobic condition Fe increased from 9.6 ppm under N^0 to 10.2 ppm under NO_3^- to 10.9 ppm under NH_4^+ and Zn content was increased from 19.5 ppm under N^0 to 20.5 ppm under NH_4^+ . In both condition Zn content is least increased in NO_3^- than NH_4^+ forms of fertilizer. This might be due to that the NH_4^+ fertilizer considerably plays the role to increased Zn in rice grain than NO_3^- fertilizer. Similarly Carlisle *et al.* (2012) and Barunawati *et al.* (2013) reported that the compared to non-fertilized and nitrate-supplied plants, the ammonium-based fertilization increased Fe contents in grains by almost 40% and those of Zn and Cu by 27 and 22% respectively.

By contrast some of the genotypes Viz; CR Dhan-40, RCPR 8, CR Dhan 201 and CGR-547 (Bargi) were showed reduced Zn under NH_4^+ which might be attributed

to the response of those particular genotypes to NO_3^- . Study found no evidence for NO_3^- forms of fertilizer for increasing or export of Fe and Zn in rice grain.

In aerobic and anaerobic condition an attempt was made to understand the genotypic relation between different form of nitrogen as well as Fe and Zn content in rice grain within population. Among these, line CR Dhan 40 contain consistently stable Zn content (in brown and polished rice grain) under different nitrogen regimes for both aerobic and anaerobic environments. In aerobic condition CGR 547 (Bargi) was showed maximum zinc 24.9 ppm and 20.6 ppm in brown and polished rice respectively under NH_4^+ form of fertilizer. In anaerobic condition maximum zinc content in brown rice was found in CR Dhan 40 with 25.6 ppm and 25.5 ppm under zero nitrogen and NO_3^- form of fertilizer respectively. Whereas R 1670-3269-2-3926-1 and Basmati- 370 shown highest zinc content 25.7 ppm and 24.9 ppm in brown rice under NH_4^+ respectively.

Among theses population majority possessed grain zinc content in polished rice ≥ 16.0 ppm which is considered as the threshold value of biofortification trial of the AICRIP (Madhu babu *et al.*, 2015). Since, harvest plus target value of zinc is 24 ppm (Harvest plus, 2013) in polished rice and the ED-XRF used in this study gives 4 ppm less than ICP which is the standard equipment for element analysis (Sanjeeva *et al.*, 2014). In present study the genotypes Basmati-370, CR 3631-1-3, CR Dhan 40, IR 83376-B-B-110-3 and RAU 1484-Aer-04 showed consistently and considerable zinc content in brown and polished rice under various forms of N fertilizer for anaerobic condition. Some researchers argued that in most agricultural soils nitrate (NO_3^-) and ammoniums (NH_4^+) are the most abundant inorganic N forms. Besides serving as N source, these two N forms do also distinctly affect many physiological processes such as changes in rhizosphere pH or in the synthesis of organic acids which, in turn, may act as micronutrient chelators (Zou *et al.*, 2001 and Marschner, 2012).

Table: 4.20.1 Mean value of iron and zinc content in rice grain under variable N regimes and environment.

	For aerobic condition					
	Fe ppm			Zn ppm		
	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺
Mean	9.1	10.4	11.3	14.1	11.9	16.1
Minimum	6.9	6.7	7.1	6.7	6.3	6.7
Maximum	12.3	16.2	20.8	20.6	21.4	24.9
SD	1.4	2.2	2.7	3.6	3.5	4.1
	For anaerobic condition					
	Fe ppm			Zn ppm		
	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺
Mean	9.6	10.2	10.9	19.5	19.4	20.5
Minimum	7.6	7.8	8.9	14.0	14.7	14.8
Maximum	12.8	13.2	13.7	25.6	25.5	25.7
SD	1.2	1.3	1.3	2.5	2.5	2.3

Table: 4.20.2 Top lines with high Zn Content in rice grain under aerobic condition.

Genotypes	Fe ppm		Zn ppm	
	Brown	Polished	Brown	Polished
Genotype with high zinc content in N⁰				
RAU 1484-Aer-04	12.3	3.2	20.6	15.3
Indira Barani Dhan 1	9.0	2.1	20.2	17.9
CR Dhan 40	9.8	3.5	20.1	18.7
Genotype with high zinc content in NO₃⁻				
CGR-547 (Bargi)	12.1	2.0	21.4	15.6
CR Dhan 40	10.6	4.5	21.0	16.6
Genotype with high zinc content in NH₄⁺				
CGR-547 (Bargi)	13.5	4.0	24.9	20.6
R 2093-1536-1-660-1	16.1	3.1	24.7	19.4
CR Dhan 40	11.7	3.1	23.8	21.7
Danteshwari	20.8	2.1	21.9	14.3

Table: 4.20.3 Top lines with high Zn Content in rice grain under anaerobic condition.

Genotypes	Fe ppm		Zn ppm	
	Brown	Polished	Brown	Polished
Genotype with high zinc content in N⁰				
CR Dhan 40	9.3	2.4	25.6	23.6
CR 3631-1-3	10.4	2.7	24.3	18.3
IR 83376-B-B-110-3	8.8	4.6	23.3	18.4
Basmati- 370	11.4	2.8	22.7	21.5
R-RF 105	11.5	3.2	22.6	19.5
CGR-547 (Bargi)	10.0	2.7	22.5	18.9
Danteshwari	10.3	2.3	21.7	16.3
RAU 1484-Aer-04	10.7	3.7	21.3	19.2
CR 3634-1-3	9.7	2.1	20.6	17.1
IR 84887-B-15	8.1	2.9	20.5	18.5
R 1902-912-2-512-1	12.1	2.5	20.4	14.8
CR Dhan 201	8.4	2.5	20.1	16.7
R 1882-306-4-243-1	10.9	2.8	20.0	15.5
R 1432-251-103-1-1	9.1	2.8	20.0	15.4
Genotype with high zinc content in NO₃⁻				
CR Dhan 40	12.2	2.7	25.5	18.4
CR 3631-1-3	12.0	3.4	23.6	19.3
RAU 1484-Aer-04	11.2	3.3	23.4	19.1
RCPR 8	12.1	3.5	23.2	22.1
CR Dhan 201	9.1	3.2	23.2	18.3
CGR-547 (Bargi)	11.2	3.3	23.1	17.6
Basmati- 370	12.7	3.7	22.7	19.1
CR Dhan 202	9.3	2.2	22.0	17.6
IR 84887-B-15	9.6	4.1	21.7	17.9
IR 83376-B-B-110-3	10.2	2.8	20.4	18.6
R-RF 105	11.1	4.1	20.3	18.6
Indira Barani Dhan 1	11.4	3.4	20.3	17.9
Genotype with high zinc content in NH₄⁺				
R 1670-3269-2-3926-1	12.3	2.6	25.7	19.5
Basmati- 370	13.7	3.2	24.9	20.6
RAU 1484-Aer-04	10.8	3.5	23.5	19.7
CR 3631-1-3	12.9	4.4	23.3	18.4
R 1902-912-2-512-1	11.4	2.3	23.2	19.1
IR 83376-B-B-110-3	9.8	2.8	22.9	20.0
CR Dhan 201	11.7	3.3	22.9	19.2
CR Dhan 202	10.8	2.6	22.5	17.6
R 2093-1536-1-660-1	12.2	2.6	22.4	15.7
CGR-547 (Bargi)	12.9	3.1	22.1	19.8
R 1700-309-1-171-1	10.0	2.8	21.7	15.3
R 1860-783-1-424-1	9.9	2.2	21.7	19.2
Indira Sona	11.2	1.9	21.4	14.5
CR Dhan 40	12.3	3.9	21.4	19.3
IR-64	10.6	3.3	21.4	16.2
IR 84887-B-15	11.5	2.9	21.1	18.5
Danteshwari	12.3	1.7	20.9	16.4
R 1779-321-1-112-1	13.5	2.2	20.6	13.8
R 1262-1667-1-1	10.7	2.3	20.5	14.3
RCPR 8	10.8	2.1	20.4	17.6
R 1882-306-4-243-1	12.6	4.9	20.3	16.4
RP 5125-2-4	11.2	2.7	20.0	18.3

4.8 Molecular diversity analysis

Molecular diversity analysis is the major criteria to assess marker value and to categories or classify rice genotypes in different heterotic group which eventually contribute to increases crop yield through heterotic breeding and progeny selection by pedigree method.

In present study total genomic DNA was extracted from 38 germplasm of rice using CTAB method. Fresh and healthy leaves were used for extraction of DNA. The DNA samples were quantified by using Nano-Drop Spectroscopy (*NANODROP 2000c*). The quantity of the samples was found in the range from 500-2000 ng/μl. DNA samples were then diluted with sterilized water such that the final concentration of DNA became 50 ng/μl. Twenty two markers were used to generate genotypic data. The details of primer used under study are presented in Table 4.21.

Genetic associations among 38 accessions were analyzed based on twenty SSR and two HvSSR markers covering all the chromosomes. Out of 22 markers, two primers were found monomorphic across all accessions. The level of polymorphism among rice cultivars was evaluated by calculating allelic number and PIC values for each of the twenty two SSR and HvSSR loci evaluated.

A total of 57 alleles were amplified and the number of alleles per locus generated by each marker ranged from 1 to 6 alleles with an average number of 2.59 alleles per locus. The results revealed that all the primers showed distinct polymorphisms among the cultivars studied indicating the robust nature of microsatellites in revealing polymorphism. Maximum number of alleles (6) was amplified by marker RM-1233.

The polymorphism information content (PIC) value across markers ranged from 0 to 0.80 with an average of 0.32. Maximum PIC on chromosome 11 was 0.80 at marker RM-1233 followed by RM-154 (0.85) and RM-1261 (0.68). Figure 4.2 showed gel pictures of amplified fragment using SSR and HvSSR primers. RM- 1233 was found as the best marker for identification of genotypes as revealed by PIC values. This finding in accordance with Martin *et al.* (2012).

Table: 4.21 Details of primers used for developing genotypic data for 38 germplasm accessions

Sr. No.	Marker	Chromosome No.	No. of Alleles	Amplicon size	Position cM	PIC	Forward sequence (5' ----->3')	Reverse sequence (5' ----->3')
1	RM-431	1	2	250-255	178.3	0.14	TCCTGCGAACTGAAGAGTTG	AGAGCAAAACCCCTGTTTCAC
2	RM-154	2	5	160-185	4.8	0.75	ACCCTCTCCGCTCGCCTCCTC	CTCCTCCTCTGCGACCGCTCC
3	RM-233	2	4	145-170	16.3	0.38	CCAAATGAACCTACATGTTG	GCATTGCAGACAGCTATTGA
4	RM-55	3	2	230-250	168.2	0.47	CCGTCGCCGTAGTAGAGAAG	TCCCGGTTATTTTAAGGGG
5	RM-307	4	2	210-250	0.0	0.05	GTACTACCGACCTACCGTTTAC	CTGCTATGCATGAACGTCTC
6	RM-161	5	2	160-175	96.9	0.10	TGCAGATGAGAAGCGGCGCCTC	TGTGTATCAGACGGCGCTCCG
7	RM-162	6	2	125-180	108.3	0.05	GCCAGCAAAACCGAGGATCCGG	CAAGGTCTTGTCGGGCTTGCGG
8	RM-454	6	1	275	99.3	0.00	CTCAAGCTTAGCTGCTGCTG	GTGATCAGTGCACCATAGCG
9	RM-588	6	2	120-125	7.4	0.39	GTTGCTCTGCCCTCACTCTTG	AACGAGCCAACGAAGCAG
10	RM-118	7	2	150-155	96.9	0.15	CCAATCGGAGCCACCGGAGAGC	CACATCCTCCAGCAGCGCCGAG
11	RM-455	7	3	125-135	65.7	0.66	AACAACCCACCACCTGTCTC	AGAAAGGAAAAGGGCTCGATC
12	RM-44	8	1	600	60.9	0.00	ACGGGCAATCCGAACAACC	TCGGGAAAACCTACCCTACC
13	RM-408	8	2	125-130	1.1	0.22	CAACGAGCTAACTCCGTCC	ACTGCTACTTGGGTAGCTGACC
14	RM-242	9	3	200-225	73.3	0.56	GGCCAACGTGTGTATGTCTC	TATATGCCAAAGACGGATGGG
15	RM-316	9	2	125-200	1.8	0.05	CTAGTTGGGCATACGATGGC	ACGCTTATATGTTACGTCAAC
16	HvSSR-10-01	10	2	400-500	0.0	0.49	ATGTATCGCTCGACAGATTT	CCGATTCAATTGATGATTCT
17	HvSSR-10-17	10	3	325-500	7.3	0.54	CGTCTTGAATCAATTTCCAT	GATTGCCCGTAGAACTATTG
18	RM-144	11	2	225-250	123.2	0.23	TGCCCTGGCGCAAATTTGATCC	GCTAGAGGAGATCAGATGGTAGTCATG
19	RM-536	11	2	300-310	42.0	0.18	TCTCTCTCTTGTTTGGCTC	ACACACCAACACGACCCACAC
20	RM-1233	11	6	150-175	170.1	0.80	TTCGTTTTCCCTTGTTAGTG	ATTGGCTCCTGAAGAAGG
21	RM-277	12	2	120-125	57.2	0.09	CGGTCAAATCATCACCTGAC	CAAGGCTTGCAAGGGAAG
22	RM-1261	12	5	205-250	112.3	0.68	GTCCATGCCCAAGACACAAC	GTTACATCATGGGTGACCCC
Mean						0.32		
			2.59					

A cluster analysis using UPGMA based on similarity coefficients was done to resolve the phylogenetic relationships among the different rice genotypes considered for the present study. The genetic similarity coefficient ranged from 0.19-1.00 as revealed by UPGMA cluster analysis using the 22 markers. Similarity index revealed that high degree of similarity in rice to the extent of 100% exists between RCPR-8 and CR-3632-1-2. Similar studies were made by different authors using SSR markers. Similar number of microsatellite markers previously used as subset for genetic diversity analysis of *Oryza sativa* by Garriss *et al.* (2005) and Thomson *et al.* (2007). Four major clusters were formed 1st cluster consist of 7 genotypes whereas 2nd cluster consisted of 28, 3rd cluster consist of 2 genotypes and in 4th cluster consist one genotype i.e. Basmati-370 which indicate dissimilarity of that genotypes with others (Fig. 4.3).

The cluster 1st consists of seven genotypes at 57% similarity and is again subdivided into four groups, among these genotypes IR-64 Drought, Indira Aerobic 1, RP-5125-2-4 and Samleshwari performed well in aerobic condition under different nitrogen regimes. The cluster 2nd was found the biggest group which contained 28 genotypes at 51 % similarity. This group again divided into 4 major subgroups. Among these two genotypes RCPR-8 and CR-3632-1-2 was found 100% similarity.

The 3rd cluster consist of two genotypes namely IR-64 and Indira Barani Dhan 1 at 52% similarity and 4th group consist only one genotype Basmati-370.

In present study the genotypes R-1779-321-1-112-1, R-1882-306-4-243-1, RCPR-8, CR-3632-1-2, CR-3631-1-3, R-RF 105 and R-1670-3269-2-3926-1 showed more than 90 % similarity. However, potential hybrid line can be produced by inter-varietal crossing based on the genetic dissimilarity value since the more the genetic dissimilarity value the more chance of getting vigorous heterosis in the progeny. Hence microsatellite marker based molecular fingerprinting could serve as a potential basis in the identification of genetically distance genotypes as well as in sorting of duplication for morphologically close accession (Martin *et al.*, 2012).

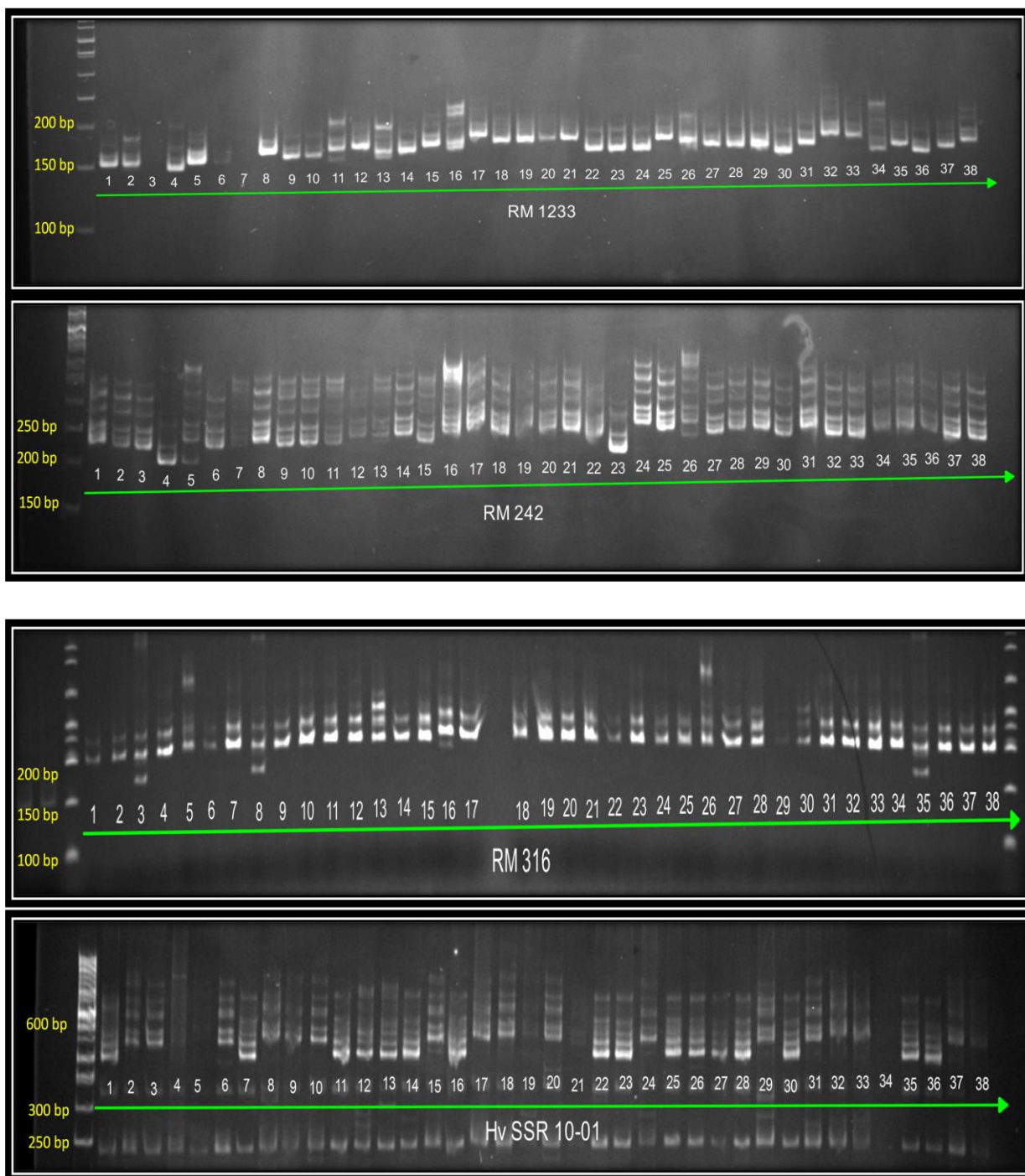


Fig. 4.2 PCR amplification of 38 germplasm accessions of rice with SSR primer RM-1233, RM-242, RM-316 and HvSSR-10-01

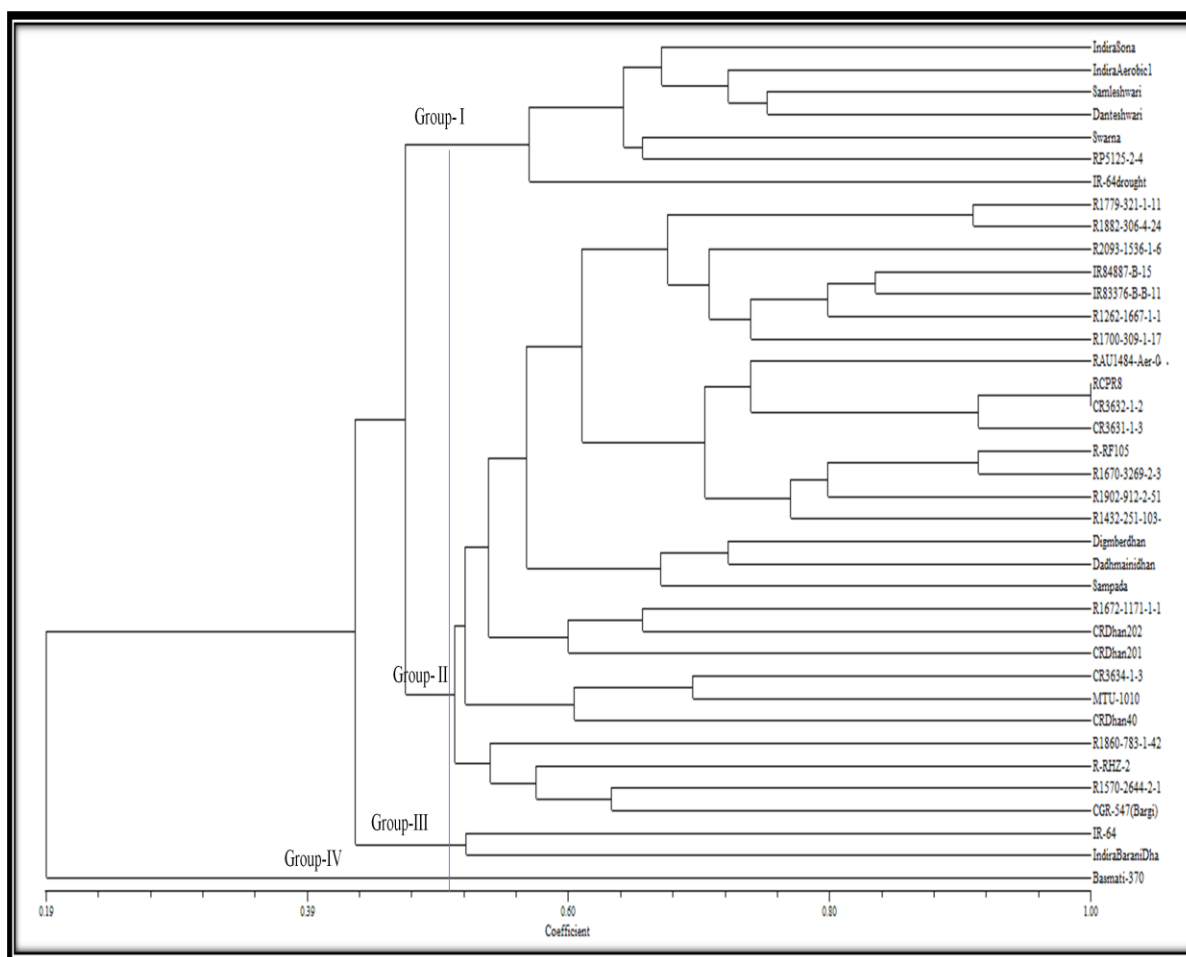


Fig. 4.3 UPGMA-based molecular dendrogram of SSR and HvSSR markers showing 38 rice germplasm

4.9 Single marker analysis

Single marker analysis is the earliest and simplest method of QTL analysis. It is based on an association between marker genotype and trait. It is likely that a QTL is close to that marker locus. Thus it finds association between marker genotype and trait. It involves regression analysis. It is used for quick scanning of the entire genome to find out best possible QTLs. It is also used to identify missing or incorrectly formatted data. There are two limitation of this method, first it underestimates QTL number and second it can't determine QTL position precisely. The concept of detecting QTLs using linked major genes was given by Sax (1923). Thoday (1961)

and Soller and Brody (1976) described the idea of using single genetic markers one at a time to systematically characterize and map individual polygene's controlling the quantitative trait.

In present study 32 selected RILs of cross between Swarna and Basmati-370 single marker analysis (SMA) was used to estimate association between marker and trait. 17 polymorphic markers were used to generate genotypic data, the details of primer and their forward and reverse sequence is given in Table 4.22. Single marker analysis (SMA) t-test is done to find out significant association between the trait and marker. The significant association was identified between markers and grain yield and its related traits.

SMA was performed for aerobic condition under N^0 , NO_3^- and NH_4^+ forms of nitrogen and the result from the Table 4.23, revealed that 2 QTLs have been identified for trait days to 50% flowering, of which 1 minor gene were found each on chromosome # 9 and #12. The marker RM-7195 was significantly linked with days to 50% flowering on chromosome # 12 under both N^0 and NO_3^- conditions.

The 4 QTLs have been identified for chlorophyll content at seedling stage of which three minor genes were found on chromosome # 9 and one gene on chromosome # 12. Under N^0 and NO_3^- conditions marker RM-24568 was significantly linked with chlorophyll content at seedling stage on chromosome # 9. Only two QTLs were identified for chlorophyll content at flowering stage, one each on chromosome # 5 and # 8. The marker RM-22710 was significantly linked with trait chlorophyll content at flowering on chromosome # 8 for NO_3^- and NH_4^+ conditions.

For the trait plant height at maturity, five QTLs have been identified, of which three minor genes were on chromosome # 5 and one each on chromosome # 8 and # 9. The two markers RM-163 and RM-18615 were significantly linked with plant height at maturity on chromosome # 5 for N^0 , NO_3^- and NH_4^+ conditions. The marker RM-22565 on chromosome # 8 and RM-24568 on chromosome # 9 was significantly linked with trait plant height under NO_3^- and NH_4^+ conditions respectively.

Table. 4.22 Details of primers used for developing genotypic data for 32 RILs population

Sr. No.	Marker	Chromosome No.	Amplicon size	Position cM	Forward sequence (5' ----->3')	Reverse sequence (5' ----->3')
1	RM-302	1	125-155	211.5	TCATGTCACTCTACCATCACAC	ATGGAGAAGATGGAAATACTTGC
2	RM-6504	1	120-135	249.9	ACCGCCTCATCTTCCGATCC	AGAGGGGTAGTATGCTCGTTGC
3	RM-12146	1	100-120	261.0	AGTATGCCCTGCCCACTACACTAGG	CAGCGAATGGCAAGAGCAACC
4	RM-163	5	150-200	123.0	ATCCATGTGCGCCTTATGAGGA	CGCTACCTCCTTCACTTACTAGT
7	RM-18615	5	115-140	122.5	CGCCTTATGAGGAGGAGATGG	AAACTCTTCGACACGCCTTGC
5	RM-18616	5	300-350	123.0	TCTAGGCAGTTGGTGTAACTCAGTGG	AACTCAAAGTCTCAAGCCATCTACAGG
6	RM-18620	5	250-270	123.2	AATCTGGAAAGTCCCTTGTACGG	AGGCTAATCACACGCTAGGTTGC
8	RM-18655	5	180-240	128.0	GGTAGGACCAAAGAGTTTGACG	GGCATCACCTTATCCAATCACCC
9	RM-408	8	125-130	0.8	CAACGAGCTAACTTCCGTCC	ACTGCTACTTGGGTAGCTGACC
10	RM-22565	8	245-265	37.2	TCCACGCGTTGTGCTAGAAATTAGC	AGCCCGAGCACCATGAACACCC
11	RM-22710	8	185-200	0.9	CGCGTGGCGGAGACTAATCG	CCTTGACTCCGAGGATTCAATTGT
12	RM-24568	9	125-130	120.0	AATAAGAGGGCGTGAGGACTGC	CCACACTATGGTTTGGTTGTCTAGC
14	RM-24571	9	255-300	120.6	AAACACATGCTGCTGACACTTGC	TTACTAGATTTACCAACGGCCCAACG
13	HvSSR-9-37	9	350-400	16.8	AATCTCAACTGCTCGGATTA	TTGATTGATTGATTGAACGA
15	RM-1233	11	148-152	170.1	TTCGTTTTCTTGTGTTAGTG	ATTGGCTCCTGAAGAAGG
16	RM-1261	12	155-195	112.4	GTCCATGCCCAAGACACAAC	GTTACATCATGGGTGACCCC
17	RM-7195	12	115-125	63.4	CGCGTGAGAGCTCCTAAAAG	TCCTTGTGTAACCTACCGCCC

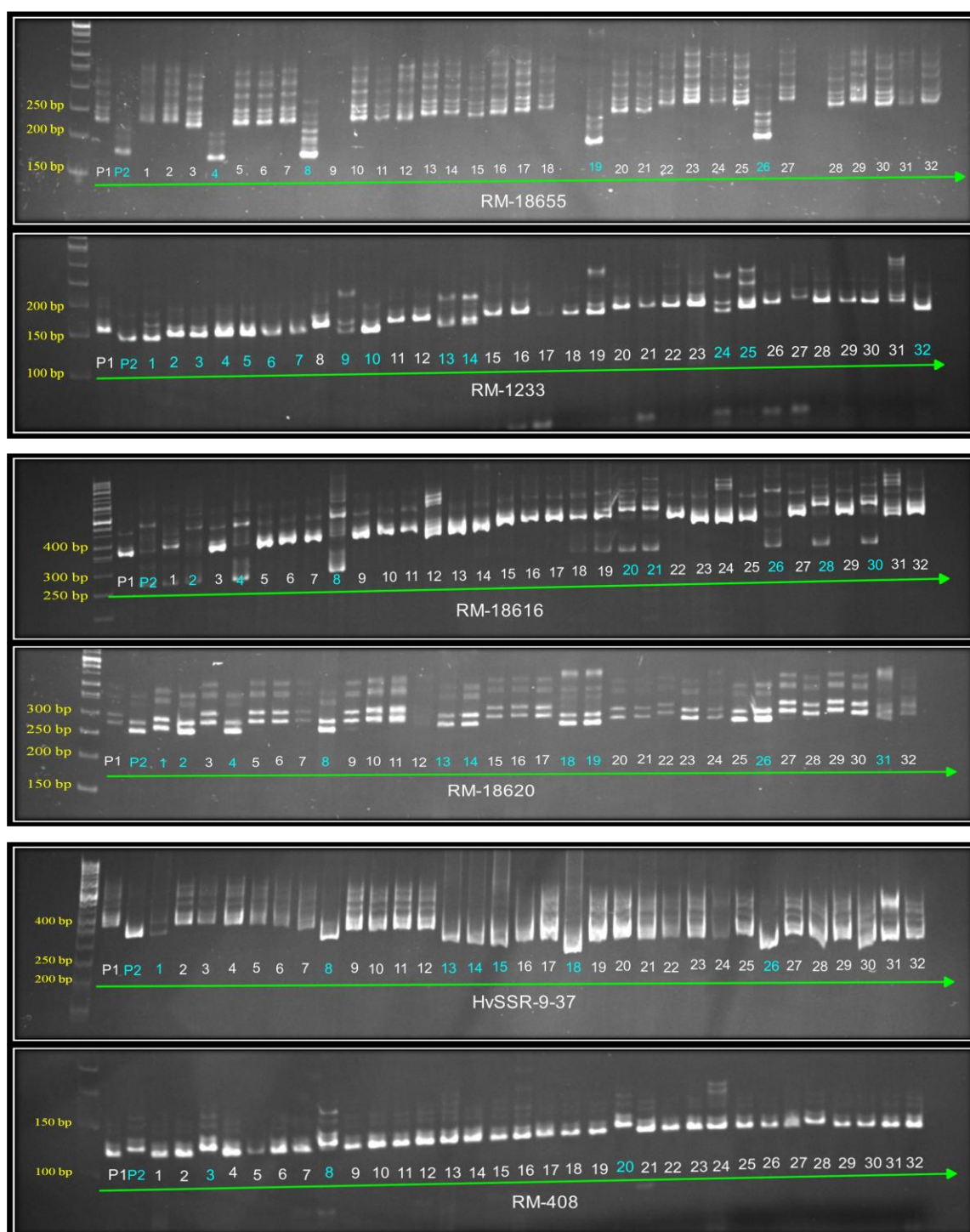


Fig.4.4 Banding pattern of RM-18655, RM-1233, RM-18616, RM-18620, HvSSR-9-37 and RM-408

The marker RM-18620 on chromosome # 5 was significantly linked with panicle length under N^0 and NH_4^+ conditions whereas RM-24568 on chromosome # 9 was significantly linked with panicle length under NO_3^- condition.

Table. 4.23 The t-test analysis of primers for grain yield and yield contributing traits

Traits	Chromosome No	Marker	t-value		
			N^0	NO_3^-	NH_4^+
DF	9	RM-24568	0.029*		
	12	RM-7195	0.017*	0.040*	
PHSD	5	RM-163	0.005**		0.026*
CCSD	9	RM-24571			0.008**
	9	HvSSR-9-37			0.031*
	9	RM-24568	0.020*	0.029*	
	12	RM-7195	0.035*		
CCFW	5	RM-18655		0.008**	
	8	RM-22710		0.047*	0.045*
PHMT	5	RM-163	0.022*	0.009**	0.045*
	5	RM-18615	0.015*	0.007**	0.025*
	5	RM-18620	0.013*		
	8	RM-22565			0.047*
	9	RM-24568		0.030*	
PL	5	RM-18620	0.017*		0.028*
	9	RM-24568		0.046*	
FGP	5	RM-18615	0.026*	0.005**	0.005**
	8	RM-22710		0.013*	
SF	5	RM-18615		0.013*	0.024*
TW	12	RM-7195			0.034*
GY	1	RM-6504			0.046*
	5	RM-18616	0.009**	0.030*	0.010*

*and ** significant at 5% and 1% respectively.

DF-Days to 50% flowering; **PHSD**-Plant height at seedling (cm); **CCSD** and **CCFW**-SPAD reading at seedling and flowering stage, respectively; **PHMT**-Plant height at maturity (cm); **PL**-Panicle length (cm); **FGP**-Number of filled grains per panicle; **SF**-Spikelet fertility (%); **TW**-Test weight (g); **GY**-Grain yield (g/m²).

Two QTLs, of which one minor gene each on chromosome # 5 and # 8 identified for the trait number of filled grains per panicle. Marker RM-18615 on chromosome # 5 was found significantly linked with number of filled grains per panicle under N^0 , NO_3^- and NH_4^+ conditions.

Under NO_3^- and NH_4^+ condition on chromosome # 5, marker RM-18615 was found significantly linked with trait spikelet fertility and under NH_4^+ condition, marker RM-7195 on chromosome # 12 was significantly linked with test weight.

Only 2 QTLs, of which one minor gene each on chromosome # 1 and # 5 have been identified for trait grain yield. Under NH_4^+ condition the marker RM-6504 on chromosome # 1 was significantly linked with grain yield whereas RM-18616 on chromosome # 5 was found significantly linked with grain yield under all conditions.

In the present study, the QTLs for grain yield and yield related traits under different nitrogen regimes for aerobic condition have been speculated and identified. These results are consistent with previous studies. Cho *et al.* (2007) found that QTLs detected under high and low N levels are widely different. Tong (2006) identified 31 QTLs that controls plant height, the number of panicles per plant, chlorophyll content, and grain yield per plant under two N conditions. Venuprasad *et al.* (2001) worked on three diverse environments and detected QTLs for ten traits at a threshold. The QTLs were spread across six chromosomes 1, 3, 4, 5, 6, and 7. Three QTLs for grain yield were detected one each on chromosome 3, 4 and 5. Wang *et al.* (2003) identified several QTLs related to grain yield in field experiments under normal N fertilization and low N-treatments. Wei *et al.* (2011) also detected QTLs for rice NUE and grain yield traits, and studied the genetic relationship between the two traits. They identified 68 QTLs for grain yield and its components under the low and normal N applications. Yue *et al.* (2006) reported 39 QTLs for productivity and spikelet fertility with RIL population of *indica* lowland $\times$ tropical *japonica* upland.

CHAPTER - V

SUMMARY AND CONCLUSIONS

In past decades, doubling of rice production has been associated with increase in the vast use of nitrogen fertilizers. The current average nitrogen use efficiency in the rice field is approximately 33%, which is poorest among cereals and a substantial proportion of the remaining 67% is lost into the environment due to drainage, volatilization, denitrification and run off. The excessive use of nitrogen fertilizers resulted in decrease of physiological nitrogen use efficiency (NUE) and cause serious environmental pollution. Nitrogen (N) is one of the most yield limiting nutrients for upland rice production. It is applied in the form of urea as it is the main nitrogen source worldwide. Predominant form of nitrogen (N) changes with change in water availability. Plant-useable N is consumed as nitrate (NO_3^-) from aerobic soils and as ammonium (NH_4^+) from flooded wetland, anaerobic soils. When the field is drained and the soil becomes aerobic, ammonium is oxidized through microbial processes (known as nitrification) into nitrate (NO_3^-). Nitrification, the conversion of ammonia (NH_3) to nitrite (NO_2^-) and then to nitrate (NO_3^-), is a dominant process in the N cycle and often determines the agronomic N use efficiency (NUE) of crops grown under unsaturated soil conditions, such as in aerobic cultivation. For the past years, attention has been made to rice breeding with high N efficiency genotypes with the awareness of environmental protection and extension of rice with high N efficiency are attempted to decrease N application. Keeping all these, the present study is conducted to study the genetics of N efficient genotypes particularly in the form of Nitrate (NO_3^-) and Ammonium (NH_4^+) over aerobic and anaerobic conditions.

During wet season 2015, set of 116 rice genotypes and seven checks were used. The augmented experimental design was used for the experiment. The field experiment was carried out under two different forms of N i.e. N in the form of calcium nitrate (NO_3^-) and N in the forms of ammonium chloride (NH_4^+) along with

zero nitrogen (N^0) for both aerobic and anaerobic condition. In another set 179 RILs between Swarna X Basmati-370 was sown in aerobic condition under different nitrogen regimes. The simple selection criteria was applied for selecting the lines and on the basis of yield performance and other important ancillary characters, 38 genotypes out of 116 were selected for further NUE study and from another set 32 RILs along with parent was used for further single marker analysis. The selected population was evaluated under wet season 2016 for various agronomical and physiological traits under different nitrogen regimes for both aerobic and anaerobic conditions. The experiment was conducted in three way factorial design. The mean data of individual lines of the population were statistically analyzed to generate overall mean and other genetic parameters viz; GCV, PCV, broad sense heritability, genetic advance and association study of the characters. The selected genotypes were also analyzed for quality parameter. In case of mapping population, phenotypic and genotypic data thus obtained from 32 RILs was used for Single marker analysis in QTL Cartographer2.5 to test the significant association between marker and grain yield.

CONCLUSIONS

- During wet season 2015, analysis of variance for augmented design revealed significant differences between test genotypes and checks for most of the characters under varied nitrogen regimes and environments.
- Based on grain yield performance, top 10 genotypes under N^0 treatment, top 15 genotypes each under NO_3^- and NH_4^+ treatment were selected for further NUE study. These genotypes showed drastic changes in grain yield amongst other genotypes under study.
- During wet season 2016, three way analyses revealed significant differences among the genotypes for all the traits indicating the presence of genetic variation among genotypes and possibility of manipulating these variations for improvement. The genotype by nitrogen ($G \times N$) interaction component was found significant for all traits under study.

- In aerobic condition highest grain yield and nitrogen use efficiency was reported by RP 5125-2-4 of 244.35, 278.82 and 310.76g/m² under N⁰, NO₃⁻ and NH₄⁺ respectively followed by IR-64 Drought (227.11, 268.17 and 300.62 g/m²) and RAU 1484-Aer-04 (200.75, 241.31 and 262.60 g/m²). While two genotypes namely Swarna and Sampada reported lowest grain yield and NUE in aerobic condition.
- The genotypes namely Indira Sona, Indira Aerobic 1, Swarna, Basmati-370 and R-1779-321-1-112-1 reported highest biological yield under N⁰, NO₃⁻ and NH₄⁺ for aerobic condition while genotype CR Dhan-40 showed lowest biological yield under all treatments for aerobic environments.
- The highest chlorophyll content was reported by R-1570-2644-2-1547-1 (40.18) under N⁰ in aerobic condition whereas R-1672-1171-1-124-1 (46.01) and R 1779-321-1-112-1 (44.50) showed highest chlorophyll content under NO₃⁻ and NH₄⁺ condition respectively.
- RCPR 8, CR 3634-1-3 and RP 5125-2-4 were reported highest grain nitrogen and protein content under N⁰, NO₃⁻ and NH₄⁺ for aerobic condition. In aerobic the maximum nitrogen harvest index was reported by CR Dhan 40 (74.56%) under N⁰ and (54.24%) under NH₄⁺ and CR 3631-1-3 (64.00%) under NO₃⁻.
- The estimated values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicated that the apparent variation is not due to genotype but also due to the influence of environment.
- High genetic advance coupled with high heritability was reported for plant height, grain yield, biological yield, harvest index, grain nitrogen yield, straw nitrogen yield, biomass nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency, nitrogen utilization efficiency and nitrogen use efficiency under differential N regimes and environments. This indicated that these traits were predominantly controlled by additive gene action and more amenable for selection.

- Harvest index followed by grain nitrogen yield, biological nitrogen yield, nitrogen harvest index, nitrogen uptake efficiency and nitrogen use efficiency exhibited positive significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions for both aerobic and anaerobic conditions.
- The characters Harvest index, grain nitrogen yield, biological nitrogen yield, nitrogen harvest index and nitrogen uptake efficiency were exhibit positive correlation along as well as showed direct effect on grain yield it reveals true relationship between them and direct selection for these traits will be rewarding for yield and NUE improvement.
- In aerobic condition traits namely, plant height, panicle length and nitrogen utilization efficiency possessed positive and significant association with grain yield under N^0 , NO_3^- and NH_4^+ conditions hence selection would be rewarding for those traits in particular environments.
- The highest root length was reported by IR-64- Drought (54.15 cm) under N^0 and Samleshwari under NO_3^- (38.35 cm) and under NH_4^+ (33.55 cm). The root length showed positive but non-significant correlation with grain yield under N^0 condition and under NO_3^- and NH_4^+ it showed negative non-significant correlation with grain yield. The character root volume exhibiting moderately positive direct effect on grain yield.
- The genotypes RP-5125-2-4 gave stable performance under different form of nitrogen for both aerobic and anaerobic condition.
- In aerobic condition the genotype RCPR-8, CR-3631-1-3, CR-3632-1-2 and in anaerobic condition the genotypes Indira Sona, RAU 1484-Aer-04, RCPR-8, CR 3631-1-3 and R-RF 105 had showed above average mean value for grain yield and $bi > 1$, indicating their suitability to favorable environment as they were highly sensitive to environmental condition.
- In aerobic condition high mean grain yield and regression $bi < 1$ were reported for genotypes Indira Sona, Digamber Dhan and Dadhmaini Dhan whereas in anaerobic condition, IR 84887-B-15, Indira Arobiec 1 and R 1672-1171-1-124-

1. These lines were suitable for cultivation in unfavorable environment as there were least sensitive environmental changes.
- In aerobic condition maximum milled kernel length was recorded in Indira Sona (6.80 mm) and CR 3634-1-3 (6.60 mm) whereas in anaerobic condition maximum kernel length was recorded in Indira Sona (7.00 mm) followed by R 2093-1536-1-660-1 and CR 3632-1-2 (6.40 mm). The highest elongation ratio was recorded in Samleshwari (1.85) and R 1672-1171-1-124-1 (1.74) for aerobic and anaerobic condition respectively.
 - The character hulling percent showed significant and positive correlation with milling and head rice recovery under both aerobic and anaerobic conditions. In both conditions kernel length showed positive and significant correlation with L/B ratio.
 - The parental lines selected from cluster VI, V and VIII for hulling , milling, head rice recovery percent, kernel length, L/B ratio, kernel length after cooking and elongation index would be used in crossing programmes to achieve desired segregants.
 - In both condition Zn content is least increased in NO_3^- than NH_4^+ forms of fertilizer. This might be due to that the NH_4^+ fertilizer considerably plays the role to increased Zn in rice grain than NO_3^- fertilizer. The genotype CR Dhan 40 contains consistently stable Zn content (in brown and polished rice grain) under different nitrogen regimes for both aerobic and anaerobic environments.
 - The polymorphism information content (PIC) value across markers ranged from 0 to 0.80 with an average of 0.32. RM- 1233 was found as the best marker for identification of genotypes as revealed by PIC values.
 - The marker RM-7195 was significantly linked with days to 50% flowering on chromosome # 12 under both N^0 and NO_3^- conditions.
 - For the trait plant height at maturity, 5 QTLs have been identified, of which 3 minor genes were on chromosome # 5 and 1 minor gene each on chromosome # 8 and # 9.

- The two markers RM-163 and RM-18615 were significantly linked with plant height at maturity on chromosome # 5 for N^0 , NO_3^- and NH_4^+ conditions.
- The 4 QTLs have been identified for chlorophyll content at seedling stage.
- Under N^0 and NO_3^- conditions marker RM-24568 was significantly linked with chlorophyll content at seedling stage on chromosome # 9.
- 2 QTLs on chromosome # 1 and # 5 have been identified for grain yield.
- RM-18616 on chromosome # 5 was found significantly linked with grain yield under all conditions.

SUGGESTIONS FOR FUTURE WORK

- The genotypes RP 5125-2-4, IR-64 (Drought) and RAU 1484-Aer-04 reported maximum grain yield and NUE for both environments hence these lines could be chosen for further study to understand the agronomic performance under different levels of nitrogen doses.
- RP 5125-2-4 was reported to have highest grain nitrogen and protein content. This genotype also showed stable performance under varied environments and can be evaluated under multi location trials for development of new variety.
- The characters Harvest index, grain and straw nitrogen, biomass, grain nitrogen yield, biological nitrogen yield, nitrogen harvest index and nitrogen uptake efficiency will be effective for the selection of NUE genotypes for future breeding programme.
- CR Dhan 40 contains consistently stable Zn content (in brown and polished rice grain) hence further confirmation is necessary to understand effect of different N form of fertilizer on Zn content in rice grain.
- CR 3631-1-3 could be used in rice breeding for the improvement of quality traits.
- On the basis of molecular diversification, the traditional variety Basmati-370 showed most diverse among material under study hence it is suggested that this variety would produce better progeny by utilization in breeding programme for quality improvement.

CHAPTER - V

REFERENCES

- Abarshahr, M., Rabiei, B. and Lahigi, H.S. 2011. Genetic variability, correlation and path analysis in rice under optimum and stress irrigation regimes. Not. Sci. Biol., 3(4): 134-142.
- Abe, A., Menker, A., Moose, S.P., Adetirimin, V.O. and Olaniyan, A.B. 2013. Genetic variation for nitrogen-use efficiency among selected tropical maize hybrids differing in grain yield potential. J. Crop Imp., 27(1): 21-52.
- Akhtar, N., Nazir, M.F., Rabnawaz, A., Mahmood, T., Safdar, M.E., Asif, M. and Rehman, A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). J. Ani. Plant Sci., 21(4): 660-664.
- Akkaya, M.S., Bhagwat, A.A. and Cregan, P.B. 1992. Length polymorphisms of simple sequence repeat DNA in soybean. Genetics, 132(4): 1131-1139.
- Akter, A., Hasan, M. J., Kulsum¹, M.U., Rahman, M.H., Paul, A.K., Lipi, L.F. and Akter, S. 2015. Genotype × environment interaction and yield stability analysis in hybrid rice (*oryza sativa* l.) by ammi biplot. Bangladesh Rice J., 19(2): 83-90.
- Allam, C.R., Jaiswal, H.K. and Qamar, A. 2015. Character association and path analysis studies of Yield and quality parameters in basmati rice (*Oryza Sativa* L.). The bioscan, 9(4): 1733-1737.
- Allard, R.W. 1960. Principles of plant breeding. John Wiley Sons Inc. New York., Pp 485.
- Anonymous, 2015. 4th Advanced estimates, Directorate of economics and statistics, Department of Agriculture Cooperation and Farmers Welfare, New Delhi, India.

- Ashikari, M., Sakakibara, H., Lin, S.Y., Yamamoto, T., Takashi, T., Nishimura, A., Angeles, E.R., Qian, Q., Kitano, H. and Matsuoka, M. 2005. Cytokinin oxidase regulates rice grain production. *Sci.*, 309: 741–745.
- Atlin, G.N., Lafitte, H.R., Tao, D., Laza, M., Amante, M. and Courtois, B. 2006. Developing rice cultivars for high-fertility upland systems in the Asia tropics. *Field Crops Res.*, 97: 43–52.
- Aulakh, M.S. and Malhi, S.S. 2005. Interactions of nitrogen with other nutrients and water: effect on crop yield and quality, nutrient use efficiency, carbon sequestration, and environmental pollution. *Int: Sparks D. L. (Ed.), Adv. in Agron.*, 21: 341–409.
- Austin A.T., Yahdjian L., Stark J.M., Belnap J., Porporato A., Norton U., Ravetta D. A. and Schaffer S. M. 2004. Water pulses and biogeochemical cycles in arid and semiarid ecosystems. *Oecologia*, 141: 221–235.
- Babu, R.C., Nguyen, B.D., Chamarerk, V., Shanmugasundaram, P., Chezian, P., Jeyaprakash, P., Ganesh, S.K., Palchamy, A., Sadasivam, S., Sarkarung, S., Wade, L.J. and Nguyen, H.T. 2003. Genetic analysis of drought resistance in rice by molecular markers: Association between secondary traits and field performance. *Crop Sci.*, 43(4): 1457-1469.
- Babu, R.V., Sandhya, K., Shobha, R.N. and Ravichandran. 2006. Genetic divergence analysis using quality traits in rice genotypes (*Oryza sativa* L.). *Oryza*, 43(4): 260-263.
- Bajpai, A. and Singh, Y. 2010. Study of quality characteristics of some small and medium grained aromatic rices of Uttar Praesh and Uttarakhand. *Agril. Sci. Dig.*, 30(4): 241-245.
- Barnard, R., Leadley, P.W. and Hungate, B.A. 2005. Global change, nitrification, and denitrification: A review. *Global Biogeochem. Cy.* 19, GB1007.
- Barracough, P.B., Howartha, J.R., Janina, J., Lopez-Bellidob, R., Parmara, S., Shepherd, C.E. and Hawkesford, M.J. 2010. Nitrogen efficiency of wheat: Genotypic and environmental variation and prospects for improvement. *European J. Agron.*, 33: 1-11.

- Barunawati, N., Ricardo, F.H.G., Bernhard, B. and Nicolaus von, W. 2013. The influence of inorganic nitrogen fertilizer forms on micronutrient retranslocation and accumulation in grains of winter wheat. *Front. Plant Sci.*, 4:320. doi:10.3389/fpls.2013.00320.
- Basten, C., Weir, B.S. and Zeng, Z.B. 1997. QTL cartographer. A reference manual and tutorial for QTL mapping. Raleigh, N.C.: Department of Statistics, North Carolina State University.
- Bernier, J., Kumar, A., Ramiah, V., Spaner, D. and Atlin, G. 2007. A large effect of QTL for grain yield under reproductive stage drought stress in upland rice. *Crop Sci.*, 47(2): 505-518.
- Bernier, J., Serraj, R., Kumar, A., Venuprasad, R., Impa, S., Veeresh Gowda, R.P., Oane, R., Spaner, D. and Atlin, G. 2009. The large-effect drought resistance QTL *qtl12.1* increases water uptake in upland rice. *Field Crop Res.*, 110(2): 139-146.
- Boopathi, N.M., Thiyagu, K., Urbi, B., Santhoshkumar, M., Gopikrishnan, A., Aravind, S., Swapnashri, G. and Ravikesavan R. 2011. Marker-assisted breeding as next-generation strategy for genetic improvement of productivity and quality: Can it be realized in cotton? *Int. J. Plant. Genomics*, 2011:670104. doi:10.1155/2011/67010.
- Broadbent, F.E., De Datta S.K. and Laureles, E.V. 1987. Measurement of nitrogen use efficiency in rice genotype. *Agron. J.*, 79: 786–791.
- Bufogele, A., Bollich, P.K., Kovar, J.L., Macchiavelli, R.E. and Lindau, C.W. 1997. Rice variety differences in dry matter and nitrogen accumulation as related to plant stature and maturity group. *J. Plant Nutri.*, 20: 1203–1224.
- Burton, G.W. 1952. Quantitative inheritance in grasses. *Proc. Sixth Int. Grassland Cong.*, 1: 227-283.
- Carlisle, E., Myers, S., Raboy, V. and Bloom, A. 2012. The effects of inorganic nitrogen form and CO₂ concentrations on wheat yield and nutrient accumulation and distribution. *Front. Plant Sci.*, 3:195. doi: 10.3389/fpls.2012.00195.

- Chaturvedi, I. 2005. Effect of nitrogen fertilizers on growth , yield and quality of hybrid rice (*Oryza Sativa* L.). *Speinger*, 6(4): 611–618.
- Cho, Y.C., Ishii, T., Temnykh, S., Chen, X., Lipovich, L., McCouch, S.R., Park, W.D., Ayres, N. and Cartinhour, S. 2000. Diversity of microsatellites derived from genomic libraries and Gen-Bank sequences in rice (*Oryza sativa* L). *Theor. Appl. Genet.*, 100(5): 713-722.
- Cho, Y.I. and Koh, H.J. 2005. Genotypic variation of physiological nitrogen use efficiency and its relationship with agronomic characters in rice. *Korean J. Breed.*, 37: 311–318.
- Cho, Y.G., Kang, H.J., Lee, J.S., Lee, Y.T., Lim, S.J., Gauch, H., Eun, M.Y. and McCouch S.R. 2007. Identification of quantitative trait loci in rice for yield, yield components, and agronomic traits across years and locations. *Crop Sci.*, 47: 2403–2417.
- Choudhury, A.T.M.A. and Kennedy, I.R. 2005. Nitrogen fertilizer losses from rice soils and control of environmental pollution problems. *Commun. Soil Sci. Plant Anal.*, 36:1625–1639.
- Coque, M and Gallais, A. 2006. Genomic regions involved in response to grain yield selection at high and low nitrogen fertilization in maize. *Theor. Appl. Genet.*, 112: 1205–1220.
- Cui, K., Huang, J., Xing, Y., Yu, S., Xu, C. and Peng, S. 2008. Mapping QTLs for seedling characteristics under different water supply conditions in rice (*Oryza Sativa* L.). *Physiologia Plantarum*, 132(1): 53-68.
- Danbaba, N., Anounye, J.C., Gana A.S., Abo, M.E. and Ukwungwu, M.N. 2011. Grain quality characteristics of Ofada rice (*Oryza sativa* L.) cooking and eating quality. *Int. Food Res. J.*, 18: 629-634.
- De Datta, S.K. and Broadbent, F.E. 1990. Nitrogen N-use efficiency of 24 rice genotypes on N-deficient soil. *Field Crops Res.*, 23: 81–92.
- Deshmukh, P.S., Kumar, A.R., Bhagat, K., Dhandapani, R., Tuti, M.D., Prakash, G., Kushwaha, S.R. and Singh, T.P. 2007. Strategies for improving abiotic stress tolerance in crop plants. *National Seminar on “Physiological and*

- molecular approaches for increasing yield and quality of Agricultural, Horticultural and Medicinal plants under changing environment*” 29th, 30th Nov. and 1st Dec. pp. 146-151.
- Devi, G.N., Ravindra Babu, V., Padmavathi, G. and Sunitha, T. 2015a. Genetic diversity in grain quality traits of rice genotypes. *J. Rice Res.*, 8 (1): 6-14.
- Devi, G.N., Padmavathi, G., Kota, S. and Babu, R.V. 2015b. Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet.*, 47(4): 424-433.
- Devienne-Barret, F., Richard-Molard, C., Chelle, M., Maury, O. and Ney, B. 2006. Ara-Rhizotron: an effective culture system to study simultaneously root and shoot development of *Arabidopsis*. *Plant and Soil*, 280: 253–266.
- Dewey, D.R. and Lu, K.H. 1959. A correlation and path co-efficient analysis of components of crested wheat grass seed production. *Agron. J.*, 15:515- 518.
- Dewi, A.K., Chozin, M.A., Triwidodo, H. and Aswidinnoor, H. 2014. Genotype x environment interaction, and stability analysis in lowland rice promising genotypes. *Int. J. Agron. Agril. Res.*, 5(5): 74-84.
- Durand, J.L., Varlet-Grancher, C., Lemaire, G., Gastal, F., and Moulia, B. 1991. Carbon partitioning in forage crops. *Acta Biotheor.*, 39: 213–224.
- Eberhart, S.A. and Russell, W.A. 1966. Stability parameters for comparing varieties. *Crop Sci.*, 6(1): 36-40.
- Edwards, M.D., Stuber, C.W. and Wendel, J.F. 1987. Molecular marker-facilitated investigation of quantitative trait loci in maize. I. Numbers, genomic distribution and types of gene action. *Genetics*, 116(1): 113-125.
- Ekka, R.E., Sarawgi, A.K. and Kanwar, R.R. 2011. Correlation and path analysis in traditional rice accessions of Chhattisgarh. *J. Rice Res.*, 4 (2):11-18.
- Engels, C., Mollenkopf, M. and Marschner, H. 1994. Effect of drying and rewetting the top soil on root growth of maize and rape in different soil types, *Z. Pflanzenernähr. Bodenk.*, 157: 139–144.
- Fageria, N.K. 2001. Nutrient management for improving upland rice productivity and sustainability. *Commun. Soil Sci. Plant Anal.*, 32: 2603–2629.

- Fageria, N.K. 2014. Nitrogen harvest index and its association with crop yields. *J. of Plant Nutri.*, 37: 795–810.
- Fageria, N.K. and Barbosa, M.P. 2001. Nitrogen use efficiency in lowland rice genotypes. *Commun. Soil Sci. Plant Anal.*, 32(13&14): 2079–2089.
- Fageria, N.K., Moreira, A. and Coelho A.M. 2011. Yield and yield components of upland rice as influenced by nitrogen sources. *J. Plant Nutri.*, 34: 361–370.
- FAOSTAT. 2016. www.fao.org/economic/RMM, Volume XIX Issue No. I.
- Farooq, M., Wahid, A., Kobayashi, N., Fujita, D. and Basra, S.M.A. 2009. Plant drought stress: Effects, mechanisms and management. *J. Sustainable Agric.*, 153–188.
- Federer, W.T. 1956. Augmented (or Hoonuiaku) Designs. *Hawaii Plr. Rec.*, 55: 191–208.
- Felix, C.W.L., Grabosky, J.C. and Bassuk, N.L. 2002. Using the SPAD 502 chlorophyll meter to assess chlorophyll and nitrogen content of Benjamin Fig and Cotton wood leaves. *Hort. tech.*, 12: 4.
- Fischer, R.A. and Hagan, R.M. 1965. Plant water relations, irrigation management and crop yield, *Exp. Agr.*, 1, 161–177.
- Fu, Q., Zhang, P., Tan, L., Zhu, Z., Ma, D., Fu, Y., Zhan, X., Cai, H. and Sun, C. 2010. Analysis of QTLs for yield-related traits in Yuanjiang common wild rice (*Oryza rufipogon* Griff.). *J. Genet. Genomics*, 37(2): 147–157.
- Gangadharaiah, S., Babu, H.N., Prasad, S.R., Pramila, C.K and Vishwanath, K. 2015. Physiochemical properties and cooking qualities of traditional rice cultivars. *Annal. Plant Sci.*, 4.8: 1173–1178.
- Garris, A.J., Thomas, H.T., Coburn, J., Krcovich, S. and McCouch, S. 2005. Genetic structure and diversity in (*Oryza sativa* L.). *Genetics*, 169:1631–1638.
- Garrity, D.P. and O'Toole, J.C. 1994. Screening rice for drought resistance at the reproductive phase. *Field Crop Res.*, 39(2-3): 99–110.
- Gholizadeh, A., Amin, M.S.M., Anuar, A.R. and Aimrun, W. 2009. Evaluation of leaf total nitrogen content for nitrogen management in a Malaysian paddy field

- by using soil plant analysis development chlorophyll meter. American J. Agril. Bio. Sci., 4(4): 278-282.
- Gnanasekaran, M., Vivekanandan, P. and Muthuramu, S. 2008. Correlation and path analysis in two line rice hybrids. Adv. Plant Sci., 21(2): 689-692.
- Gomez, M., Babu, R.C., Shanmugasundaram, P., Satheesh Kumar, R., Suresh, R., Biji, K.R., Boopathi, N.M., Jeyaprakash, P., Gurumurthy, S. and Price, A.H. 2005. QTL mapping and marker assisted selection for drought tolerance in rice (*Oryza sativa* L.). In: *Proceedings of the 2nd International Conference on Integrated Approaches to Sustain and Improve Plant Production under Drought Stress*. University of Rome, “La Sapienza”, Rome, Italy, September 24-28: pp. 6-19.
- Gomez, S.M., Kumar, S.S., Jeyaprakash, P., Suresh, R., Biji, K.R., Boopathi, N.M., Price, A.H. and Babu, R.C. 2006. Mapping QTLs linked to Physio-Morphological and plant production traits under drought stress in rice (*Oryza sativa* L.) in the target environment. American. J. Biochem. Biotech., 2(4): 161-169.
- Gomez, S.M., Manikanda Boopathi, N., Satheesh Kumar, S., Ramasubramanian, T., Chengsong, Z., Jeyaprakash, P., Senthil, A. and Babu, R.C. 2010. Molecular mapping and location of QTLs for drought-resistance traits in indica rice (*Oryza sativa* L.) lines adapted to target environments. Acta Physiol. Plant, 32(2): 355-364.
- Gonzalez-Dugo V., Durand J.L., Gastal F. and Picon-Cochard C. 2005. Short-term response of the nitrogen nutrition status of tall fescue and Italian ryegrass swards under water deficit, Australian. J. Agri. Res., 56: 1269–1276.
- Gopikannan, M. and Ganesh, S.K. 2013. Inter-Relationship and path analysis in rice (*Oryza sativa* L.) under Sodicty. Indian J. Sci. Technol., 6(9): 5223-5227.
- Gorissen, A., Tietema, A., Joosten N.N., Estiarte M., Peñuelas, J., Sowerby, A., Emmett B.A. and Beier, C. 2004. Climate change affects carbon allocation to the soil in shrublands. Ecosystems, 7: 650–661.

- Guingo, E., Herbert, Y. and Charcosset, A. 1998. Genetic analysis of root traits in maize. *Agronomie*, 18: 225–235.
- Gujer, W. 2010. Nitrification and me – A subjective review. *Water Res.*, 44, 1-19.
- Haefele, S.M., Jabbar, S.M.A., Siopongco, J.D.L.C., Tirol-Padre, A., Amarante, S.T., Sta Cruz, P.C. and Cosico, W.C. 2008. Nitrogen use efficiency in selected rice (*Oryza sativa* L.) genotypes under different water regimes and nitrogen levels. *Field Crops Res.*, 107: 137–146.
- Haider, Z., Khan A.S. and Zia, S. 2012. Correlation and path coefficient analysis of yield components in rice (*Oryza sativa* L.) under simulated drought stress condition. *American-Eurasian J. Agr. Environ. Sci.*, 12(1): 100-104.
- Hakeem, K.R., Chandna, R., Altaf, A. and Muhammad, I. 2012. Physiological and molecular analysis of applied nitrogen in rice genotypes. *Rice Sci.*, 19: 213–222.
- Hamam, K.A. and Khaled, G.A.S.A. 2009. Stability of wheat genotypes under different environments and their evaluation under sowing dates and nitrogen fertilizer levels. *Australian J. Basic App. Sci.*, 3(1): 206-217.
- Hamaoka, N., Uchida, Y., Tomita, M., Kumagai, E., Araki, T. and Ueno, O.O. 2013. Genetic variations in dry matter production, nitrogen Uptake and nitrogen use efficiency in the AA Genome *Oryza* species grown under different nitrogen conditions. *Plant Prod. Sci.*, 16(2): 107—116.
- Hanson, W.D., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating population Korean Lespandeza. *Agron. J.*, 48(6): 268-272.
- Haque, M.A. and Haque, M.M. 2016. Growth, yield and nitrogen use efficiency of new rice variety under variable nitrogen rates. *Scientific Research*, 7(3): 612-622.
- Hassan, M.J., Rasul, M.G., Mian, M.A.K., Hasanuzzaman, M. and Chowdhury, M.M.H. 2000. Genetic divergence of yam. *Bangladesh J. Plant Breed. Genet.*, 13 (1):07-11.

- Hassan, M.S., Khair, A., Azad, M.M.H.A.K. and Hamid, A. 2009. Genotypic variation in traditional rice varieties for chlorophyll content, SPAD value and nitrogen use efficiency. *Bangladesh J. Agril. Res.*, 34(3): 505-515.
- Hosen, S., Siddiquee, M.A., Jahan, S., Alam, M.S., Hoque, F., Bhowmick, S., Ferdous, N and Shozib, H.B. 2016. Physicochemical properties of Aus cultivars in Bangladesh. *Biores. Comm.*, 2(1): 200-204.
- Hossain, M.A., Hamid, A., Hossain, S.M.A. and Bhuiyan, N.I. 2003. Genetic divergence and path analysis in groundnut. *Bangladesh J. Plant Breed. Genet.*, 16 (1): 9-15.
- Hossain, M.S., Singh, A.K. and Fasih-uz-Zaman. 2009. Cooking and eating characteristics of some newly identified inter sub-specific (indica/japonica) rice hybrids. *Science Asia*, 35: 320-325.
- Huang, B. and Gao, H. 2000. Root physiological characteristics associated with drought resistance in tall fescue cultivars. *Crop Sci.*, 40: 196–203.
- Huang, M., Jiana, C., Fangbo, C., Ligeng, J., Yingbin, Z. and Guofu, D. 2016. Improving physiological N-use efficiency by increasing harvest index in rice: a case in super-hybrid cultivar Guiliangyou 2. *Archi. Agron. Soil Sci.*, 62 (5):725–743.
- Huggins, D.R. and Pan, W.L. 2003. Key indicators for assessing nitrogen use efficiency in cereal-based agroecosystems. *J. Crop Prod.*, 8: 157–185.
- Ingram, K.T., Bueno, F.D., Namuco, O.S., Yambao, E.B. and Beyrouty, C.A. 1994. Rice root traits for drought resistance and their genetic variation, *Rice Roots. Nutrient and Water Use*, 67–77.
- Inthapanya, P., Sihavong, P., Sihathap, V., Chanphengsay, M., Fukai, S. and Basnayake, J. 2000. Genotype differences in nutrient uptake and utilisation for grain yield production of rainfed lowland rice under fertilised and non-fertilised conditions. *Field Crops Res.*, 65: 57-68.
- IRRI (International Rice Research Institute). 1984. Terminology for rice growing environments. Los Banos, Philippines: International Rice Research Institute.

- Isfan, D. 1993. Genotypic variability for physiological efficiency index of nitrogen in oats. *Plant and Soil*, 154: 53–59.
- Islam, M.S., Bhuiya, M.S.U., Rahman, S. and Hussain, M.M. 2009. Evaluation of SPAD and LCC based nitrogen management in rice . *Bangladesh J. Agril. Res.*, 34(4): 661-672.
- Islam, M.R., Haque, K.M., Akter, N. and Karim, M.A. 2014. Leaf chlorophyll dynamics in wheat based on SPAD meter reading and its relationship with grain yield. *Scientia Agriculturae*, 8 (1): 13-18.
- Jiang, L.G., Dai, T.B., Wei, S.Q., Gan, X.Q., Xu, J.Y. and Cao, W.Q. 2003. Genotypic differences and valuation in nitrogen uptake and utilization efficiency in rice. *Acta Phytoecol Sin.*, 27(4): 466–471. (In Chinese with English abstract).
- Jiang, L., Dong, D., Gan, X. and Wei, S. 2005. Photosynthetic efficiency and nitrogen distribution under different nitrogen management and relationship with physiological nitrogen use efficiency in three rice genotypes. *Plant Soil.*, 271:321-8; [http:// dx.doi.org/10.1007/s11104-004-3116-9](http://dx.doi.org/10.1007/s11104-004-3116-9).
- Johnson, H.W., Robinson, H.P. and Comstoc, R.E. 1955. Estimation of genetic and environmental variability in soybeans. *Agron. J.*, 47: 314-318.
- Jonaliza, C., Lanceras, P., Pantuwan, G., Boonrat, J. and Theerayut, T. 2004. Quantitative trait loci associated with drought tolerance at reproductive stage in rice. *Plant Physio.*, 135:1–16.
- Jongdee, B., Mitchell, J.H. and Fukai, S. 1997. Modeling approach for estimation of rice yield reduction due to drought in Thailand. In S Fukai, M Cooper, J Salisbury, eds, *Breeding Strategies for Rainfed Lowland Rice in Drought-Prone Environments. Proceedings of an International Workshop*, Ubon Ratchathani, Thailand, November 5–8, 1996. ACIAR Proceedings No. 77, pp 65–73.
- Juliano, B.O. and Villareal, C.P. 1993. Grain quality evaluation of world rice. International Rice Research Institute, Manila, Philippines.

- Kamara, A.Y., Kling, J.G., Menkir, A. and Ibikunle, G. 2003. Agronomic performance of maize (*Zea mays* L.) breeding lines derived from a low nitrogen maize population. *J. Agri. Sci.*, 14: 221–230.
- Kang, S.G., Hassan, M.S., Ku, B., Sang, W. G., Choi, M. K., Kim, Y. D., Park, H. K., Chowdhury, M., Kim, B.K. and Lee, J.H. 2013. Nitrogen use efficiency of high yielding japonica rice (*oryza sativa* L.) influenced by variable nitrogen applications. *Korean J. Crop Sci.*, 58(3): 213-219.
- Karim, D.U., Sarkar, M.N.A., Siddique, M.A., Khaleque, M. and Hasnat, M.Z. 2007. Variability and genetic parameter analysis in aromatic rice. *Int. J. Sustain. Crop Prod.*, 2(5): 15-18.
- Karmakar, J., Roychowdhury, R., Kar, R.K., Deb, D. and Dey, N. 2012. Profiling of selected indigenous rice (*Oryza sativa* L.) landraces of Rarh Bengal in relation to osmotic stress tolerance. *Physiol. Mol. Biol. Plants.*, 18(2):125–132.
- Keller, M. 2005. Deficit irrigation and vine mineral nutrition. *Am. J. Enol. Viticult.*, 56: 267–283.
- Khatun, M.M., Hazrat, A.M., Quirio, D. and Cruz, N.D. 2003. Correlation studies on grain physicochemical characteristics of aromatic rice. *Pakistan J. Bio. Sci.*, 6(5): 511-513.
- Khatun, M.T., Hanafi, M.M., Yusop, M.R., Wong, M.Y., Salleh, F.M. and Ferdous, J. 2015. Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. *Bio. Med. Res. Int.*, <http://dx.doi.org/10.1155/2015/290861>.
- Kiani, G. 2013. Heritability and diversity analysis of quantitative traits in rice. *Agri. Cons. Scienti.*, 78(2): 113-117.
- Koffi, D., Boubie, V.B. and Valere, C.M. 2016a. Effect of nitrogen fertilizer on yield and nitrogen use efficiency of four aromatic rice varieties. *Emir. J. food agric.*, 28(2): 126-135.

- Koffi, D., Vincent, B. B. and Valere, M. 2016b. Yield and nitrogen use efficiency of aromatic rice varieties in response to nitrogen fertilizer. *Emir. J. food agric.*, 28 (2): 126-135.
- Koli, N.R. and Chandra, P. 2012. Genotype X environment interactions and adaptability with sustainability index their comparison in aromatic rice (*Oryza sativa* L.) under transplanted condition. *Int. J. Agric. Environ. Biotech.*, 5(4): 401-404.
- Kondo, M., Pablico, P.P., Aragones, D.V., Agbisit, R., Morita, S. and Courtois, B. 2003. Genotypic and environmental variations in root morphology in rice genotypes under upland field conditions. *Plant and Soil*, 255: 189–200.
- Konnerup, D. and Brix, H. 2010. Nitrogen nutrition of *Canna indica*: effects of ammonium versus nitrate on growth, biomass allocation, photosynthesis, nitrate reductase activity and N uptake rates. *Aquat. Bot.*, 92: 142–148.
- Kota, S., Singh, S.S., Mohapatra, T., Singh, A.M., Brajendra, B.V.P. and Ravichandran, S. 2013. Genotype x environment interaction analysis for grain yield in new plant type (npt) wheat derivatives. *SABRAO J. Breed. Genet.*, 45 (3): 382-390.
- Kumar, R., Malaiya, S. and Shrivastava, M.N. 2004. Evaluation of morpho-physiological traits associated with drought tolerance in rice. *Indian J. Pl. Physi.*, 9(3): 305-307.
- Kumar, A., Bernier, J., Verulkar, S., Lafitte, H.R. and Atlin, G.N. 2008. Breeding for drought tolerance: direct selection for yield, response to selection and use of drought-tolerant donors in upland and lowland-adapted populations. *Field Crop Res.*, 107(3): 221-231.
- Kumar, N., Mathpal, B., Sharma, A. and Shankdhar, S.C. 2014. Physiological evaluation of nitrogen use efficiency and yield attributes in rice (*Oryza sativa* L.) genotypes under different nitrogen levels. *Cereal Res. Commun.*
- Kumar, V., Koutu, G.K., Singh, S.K., Mishra, D.K., Singh, P.K. and Sohgaure, N. 2014. Genetic analysis of inter sub-specific derived mapping population

- (RILs) for various yield and quality attributing traits in rice. *Int. Sci. J.*, 1(3): 2348 – 6058.
- Kumari, S., Kewat, R.N., Singh, R.P. and Singh, P. 2013. Studies of quality characteristics in short grain scented rice (*Oryza sativa* L.) varieties accessions. *Trends in Biosci.*, 6(2): 177-179.
- Ladha, J.K., Kirk, G.J.D., Bennett, J., Peng, S., Reddy, C.K., Reddy, P.M. and Singh, U. 1998. Opportunities for increased nitrogen-use efficiency from improved lowland rice germplasm. *Field Crops Res.*, 56: 41–71.
- Lafitte, H.R., Ismail, A. and Bennet, A. 2004a. Abiotic stress tolerance in rice for Asia: Progress and the future. *In: Fischer, T. et al. (Eds.) New directions for a diverse planet: Proceedings of the 4th International Crop Science Congress*, Brisbane, Australia.
- Lafitte, H.R., Price, A.H. and Courtois, B. 2004b. Yield response to water deficit in an upland rice mapping population: associations among traits and genetic markers. *Theor. Appl. Genet.*, 109(6): 1237-1246.
- Lakew, T. 2015. Estimation of genetic variability and trait association in nitrogen use efficiency of upland rice varieties in North Western Ethiopia. *Int. J. Res. Rev.*, 2 (9): 527-535.
- Lanceras, J.C., Pantuwan, G., Jongdee, B. and Toojinda, T. 2004. Quantitative trait loci associated with drought tolerance at reproductive stage in rice. *Plant Physiol.*, 135: 384–399.
- Laperche, A., Brancourt-Hulmel, M., Heumez, E., Gardet, O. and Le Gouis, J. 2006. Estimation of genetic parameters of a DH wheat population grown at different N stress levels characterized by probe genotypes. *Theor. Appl. Genet.*, 112: 797–807.
- Lemaire, G., Recous, S. and Mary B. 2004. Managing residues and nitrogen in intensive cropping systems. New understanding for efficient recovery by crops. *Int: Fischer, T., Turner, N. C., Angus, J. F., McIntyre, L., Robertson, M. J., Borrell, A., Lloyd, D. (Ed), 4th International Crop Science Congress*, The Regional Institute Ltd, Gosford, Brisbane, Australia.

- Li, H., Ye, G. and Wang, J. 2007. A modified algorithm for the improvement of composite interval mapping. *Genetics*, 175(1): 361-374.
- Li, Z. K. and Xu, J. L. 2007. Breeding for drought and salt tolerant rice (*Oryza sativa* L.): progress and perspectives. In: Jenks, M. A. (Ed) on Advances in molecular breeding toward drought and salt tolerant crops. Springer, USA,: 531-564.
- Li, S.X., Wang, Z.H., Hu, T.T., Gao, Y.J. and Stewart, B.A. 2009. Nitrogen in dry land soils of china and its management. Int: Sparks, D. L. (Ed), Adv. Agronomy, 123–181.
- Lincoln, S., Daly, M. and Lander, E. 1992. Mapping genes controlling quantitative traits with MAPMAKER/ QTL. Whitehead Institute Technical Report.
- Liu, G., Mei, H., Liu, H., Yu, X., Zou, G. and Luo, L. 2010. Sensitivities of rice grain yield and other panicle characters to late-stage drought stress revealed by phenotypic correlation and QTL analysis. *Mol. Breed.*, 25(4): 603-613.
- Madhu Babu, P., Praveen, V., Sai, S. M., Sanjeeva Rao, D., Surekha, K., Sundaram, R.M., Ravindra Babu, V. and Neeraja, C.N. 2015. Association of OsYSL9 gene with high iron and zinc content in rice grains and identification of elite rice lines. *Int. J. Tro. Agri.*, 33 (4): 3031-3036.
- Makhziah, Kusningrum, R. and Hery, P. 2013. Effect of nitrogen supply and genotypic variation for nitrogen use efficiency in maize. *American J. Exper. Agri.*, 3(1): 182-199.
- Makwana, B. P., Jadeja, G. C., Patel, C. G., Patel, R. M. and Gami, R. A. 2010. Path analysis of qualitative and quantitative characters in slender grain rice (*Oryza sativa* L.). *Int. J. Plant Sci.*, 5 (1): 294-296.
- Malik, T.H., Lal, S.B., Wani, N.R., Amin, D. and Wani, R.A. 2014. Effect of different levels of nitrogen on growth and yield attributes of different varieties of basmati rice (*Oryza Sativa* L.). *Int. J. Sci. Tec. Res.*, 3(3): 444-448.
- Mambani, B. and Lal, R. 1983. Response of upland rice varieties to drought stress - II. Screening rice varieties by means of variable moisture regimes along a toposequence. *Plant Soil*, 73: 73–94.

- Manly, K.F. and Elliott, R.W. 1991. RI manager: A microcomputer program for analysis of data from recombinant inbred strain. *Mamm. Genome*, 1(2): 123-126.
- Manzoor, Z., Awan, T.H., Zahid., M.A. and Faiz, F.A. 2006. Response of rice crop (super basmati) to different nitrogen levels. *J. Anim. Plant Sci.*, 16: 1–2.
- Marschner, P. 2012. Marschner's mineral nutrition of higher plants. San Diego, CA: Academic Press.
- Masclaux-Daubresse, C. and Chardon, F. 2011. Exploring nitrogen remobilization for seed filling using natural variation in *Arabidopsis thaliana*. *J. Exp. Bot.*, 62: 2131–42.
- Martin, S., Ashrafuzzaman, M., Md. Islam, M., Sikdar, S. U. and Zobayer, N. 2012. Molecular marker based (SSR) genetic diversity analysis in deep water rice germplasms of bangladesh. *Int. J. Biosci.*, 10(2):64-72.
- McCouch, S.R., Kochert, G., Yu, Z.H., Wang, Z.Y., Khush, G.S., Coffman, R.W. and Tanksley, S.D. 1988. Molecular mapping of rice chromosomes. *Theor. Appl. Genet.*, 76(6): 815-829.
- McCouch, S.R., Chen, X., Panaud, O., Temnykh, S., Xu, Y., Cho, Y.G., Huang, N., Ishii, T. and Blair, M. 1997. Microsatellite marker development, mapping and applications in rice genetics and breeding. *Plant Mol. Biol.*, 35(1-2): 89-99.
- McCouch, S.R., Teytelman, L., Xu, Y., Lobos, K.B., Clare, K., Walton, M., Fu, B., Maghirang, R., Li, Z., Xing, Y., Zhang, Q., Kono, I., Yano, M., Fjellstrom, R., DeClerck, G., Schneider, D., Cartinhour, S., Ware, D. and Stein, L. 2002. Development and mapping of 2240 new SSR markers for rice (*Oryza sativa* L.). *DNA Res.*, 9(6): 199-207.
- Mei-Hua, D., Xiao-Jun, S., Yu-Hua, T., Bin, Y., Shao-Lin, Z., Zhao-Liang, Z. and Kimura, S.D. 2012. Optimizing nitrogen fertilizer application for rice production in the Taihu Lake Region, China. *Pedosphere*, 22(1): 48–57.

- Mohan, M., Nair, S., Bhagwat, A., Krishna, T.G., Yano, M., Bhatia, C.R. and Sasaki, T. 1997. Genome mapping, molecular markers and marker-assisted selection in crop plants. *Mol. Breed.*, 3: 87-103.
- Mohankumar, M.V., Sheshshayee, M.S., Rajanna, M.P. and Udayakumar, M. 2011. Correlation and path analysis of drought tolerance Traits on grain yield in rice germplasm accessions. *ARPN J. Agric. Bio. Sci.*, 6(7):70-77.
- Moll, R.H., Kamprath, E.J. and Jackson, W.A. 1982. Analysis and interpretation of factors which contribute to efficiency of nitrogen utilization. *Agron. J.*, 74: 562-564.
- Moosavi, M., Ranjbar, G., Zarrini, H.N. and Gilani A. 2015. Correlation between morphological and physiological traits and path analysis of grain yield in rice genotypes under Khuzestan conditions. *Biol. Forum. Int. J.*, 7(1): 43-47.
- Mosavi, A.A., Babaiean, N.J. and Kazemitabar, K. 2013. Environmental responses and stability analysis for grain yield of some rice genotypes. *World Appl. Sci. J.*, 21 (1): 105-108.
- Murthy, B. R. and Arunachalam, V. 1966. The nature of genetic divergence in relation to breeding system in some crop plants. *Indian J. Genetics*, 26:188- 198.
- Namai, S., Toriyama, K. and Fukuta, Y. 2009. Genetic variations in dry matter production and physiological nitrogen use efficiency in rice (*Oryza sativa* L.) varieties. *Breed. Sci.*, 59: 269-76;
- Nandan, R., Sweta and Singh, S.K. 2010. Character association and path analysis in rice (*Oryza sativa* L.) genotypes. *World J. Agric. Sci.*, 6 (2): 201-206.
- Naveen Kumar, V. M. and Uma, M. S. 2016. Genetic variability for nitrogen use efficiency and yield related traits in rice under low nitrogen and Available soil nitrogen conditions. *Int. J. Appl. Pure Sci. Agri.*, 2(7):83-90.
- Nelson, J.C. 1997. Q GENE: Software for marker based genomic analysis and breeding. *Mol. Breed.*, 3(3): 239-245.
- Nie. L., Peng, S., Bouman, B.A.M., Visperas, R.M., Huang, J. and Cui, K. 2008. Alleviation of soil sickness caused by aerobic monocropping: growth response of aerobic rice to nutrient supply. *Field Crops Res.*, 107:129–136.

- Nie, Y.Y., Zhang, L., Wu, Y.H., Liu, H.J., Mao, W.W., Du, J., Xiu, H.L., Wu, X.Y., Li, X., Yan, Y.W., Liu, G.L., Liu, H.Y. and Hu, S.P. 2015. Screening of candidate genes and fine mapping of drought tolerance quantitative trait loci on chromosome 4 in rice (*Oryza sativa* L.) under drought stress. *Ecol. Evol.*, 5(21): 5007-5015.
- Oji, Y. and Izawa, G. 1970. Studies on the absorption and assimilation of inorganic nitrogen in intact plants (part 2). Physiological characteristics in absorption and assimilation of nitrate-N and ammonium-N in young rice seedlings. *J. Sci. Soil Manure Jpn.*, 41: 31–36.
- Oliver, M.J., Guo, L., Alexander, D.C., Ryals, J.A., Wone, B.W.M. and Cushman, J. C. 2011. A sister group metabolomic contrast using untargeted global metabolomic analysis delineates the biochemical regulation underlying desiccation tolerance in *Sporobolus stapfianus*. *Plant Cell*, 23: 1231-1248.
- Onillon B., Durand J. L., Gastal F. and Tournebize, R. 1995. Drought effects on growth and carbon partitioning in a tall fescue sward grown at different rates of nitrogen fertilization, *Eur. J. Agron.*, 4: 91–99.
- Pachauri, V., Nilay, T., Vikram, P., Singh, N.K. and Singh, S. 2013. Molecular and morphological characterization of Indian farmer rice varieties. *Aus. J. of Crop Sci.*, 7(7): 923-932.
- Panda, S.C., Panda, P.C. and Nanda, S.S. 1995. Effect of level of N and P on yield and nutrient uptake of rice. *Oryza.*, 32:18-20.
- Pantuwan, G., Fukai, S., Cooper, M., Rajatasereekul, S. and O'Toole, J.C. 2002. Yield response of rice (*Oryza sativa* L.) genotypes to drought under rainfed lowland and selection of drought resistant genotypes. *Field Crop Res.*, 73(2-3): 169-180.
- Panwar, L.L., Joshi, V.N. and Ali, M. 2008. Genotype $\times$ environment interaction in scented rice. *Oryza*, 45(2): 103-109.
- Parikh, M., Rastogi, N.K., and Sarawgi, A.K. 2012. Variability in grain quality traits of aromatic rice (*oryza sativa* L.). *Bangladesh J. Agril. Res.*, 37(4): 551-558.

- Park, H. and Mok, S.K. 1975. Nitrogen efficiency and its relation to various physiological characteristics among rice varieties. J. Korean Agric. Chem. Soc., 8: 105–111.
- Pirmoradian, N., Sepaskhah, A.R. and Maftoun, M. 2004. Deficit irrigation and nitrogen effects on nitrogen-use efficiency and grain protein of rice. Agronomie, 24: 143–153.
- Prakash, A., Mandal, L. and Verulkar, S.B. 2015. The association of markers with Drought Susceptibility Index (DSI) in rice (*Oryza sativa* L.). Europ J. Biotech. Biosci., 3(2): 10-14.
- Prudente, J. A., Gilbert C. Sigua, G. C., Kongchum, M. and Alfredo, D. 2008. Improving yield and nutrient uptake potential of japonica and indica rice varieties with nitrogen fertilization. World J. Agril. Sci., 4 (4): 427-434.
- Puckridge, D.W. and O'Toole, J.C. 1980. Dry matter and grain production of rice, using a line source sprinkler in drought studies. Field Crop Res., 3: 303-319.
- Rajesh, T., Paramasivam, K. and Thirumani, S. 2010. Genetic divergence in land races of rice. Ele. J. Plant Breed., 1 (2):199-204.
- Rajeshwari, S. and Nadarajan, N. 2004. Correlation between yield and yield components in rice (*Oryza sativa* L.). Agric. Sci. Dig., 24:280-282.
- Ramaiah K.1969. Grain Classification page No. 629 - Rice Research in India, ICAR Publication, 1985.
- Rao, K.J., Rao, A.U., Sekhar, D., Ramu, P.S. and Rao, N.V. 2014. Effect of different doses of nitrogen on performance of promising varieties of rice in high altitude areas of Andhra Pradesh. Int. J. Farm Sci., 4(1): 6-15.
- Ravindra Babu V. 2013. Importance and advantages of rice biofortification with iron and zinc. Journal of SAT., Agricultural Research 11.
- Robinson, H. F. 1996. Quantitative genetics in relation to breeding on the centennial of mendelian. Indian J. Genet., 26: 171-187.

- Row, S.K. and Venkateswarlu, B. 1983. Influence of varied moisture regime of different growth phase on yield component in rice. *Indian J. Plant Physiol.*, 26: 126-132.
- Roy, S., Biswar, A., Tarafdar, J. and Senapati, B.K. 2007. Genetic divergence of rice germplasm for morphological and quality characters. National symposium on rice, held at CRRI, Cuttack 2007.
- Sadras, V. O. 2005. A quantitative top-down view of interactions between stresses: theory and analysis of nitrogen-water co-limitation in Mediterranean agro-ecosystems. *Aust. J. Agri. Res.*, 56: 1151–1157.
- Samonte, S.O.P.B., Lloyd, T.W., James, C.M., Shannon, R.M.P., Anna, M.M C. and Jovenio, S.L. 2006. Nitrogen Utilization Efficiency: relationships with grain yield, grain protein, and yield-related traits in rice. *Agron. J.*, 98:168-176.
- Samrat, G.D.S., Singh, G.P., Singh, A.M., Deveshwar, J.J. and Arvind, A. 2010. Stability analysis for physiological and quality parameters in wheat (*Triticum aestivum*). *Indian J. Agric. Sci.*, 80 (12): 1028–1032.
- Sanjeeva Rao, D.P., Mbadhu Babu., Sawrnalatha, P., Suncetha Kota, V.P., Baadana, G.S., Varaprasad, K.S., Neeraja and Ravindra Babu. 2014. Assessment of grain zinc and iron variability in rice germplasm using Energy Dispersive X-ray Fluorescence Spectrophotometer (ED-XRF). *J. Rice Res.*, 71 and 2: 45-52.
- Sarawgi, A.K., Parikh, M. and Sharma, B. 2012. Agro-Morphological and quality characterization of Dubraj group from aromatic rice germplasm of Chhattisgarh and Madhya Pradesh. *Int. J. of Plant Res.*, 25(2): 387- 394.
- Sarkar, K.K., Bhutia, K.S., Senapati, B.K. and Roy, S.K. 2007. Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). *Oryza*, 44(1): 64-67.
- Satheeshkumar, P. and Saravanan, K. 2012. Genetic divergence analysis for grain yield and quality traits in rice (*Oryza sativa* L.). *Plant Archiv.*, 12(2):639-644.

- Sattelmacher, B., Horst, W.J. and Becker, H.C. 1994. Factors that contribute to genetic variation for nutrient efficiency of crop plants. *Z. Pflanzen. Bodenk*, 157: 215–24.
- Sawant, D.S., Kunkerkar, R.L., Shetye, V.N. and Shirdhankar, M.M. 2005. Stability assessment in late duration rice hybrids. In: *national seminar on “Rice and Rice Based Systems for Sustainable Productivity, Extended summaries”*, ICAR Research Complex for Goa, 18-19th October; 75-76.
- Sax, K. 1923. The association of size difference with seed coat pattern and pigmentation in *Phaseolus vulgaris*. *Genetics*, 8(6): 552-560.
- Searle, S.R. 1961. Phenotypic, genotypic and environmental correlations. *Biometrics*, 17(3): 474-780.
- Seo, J.H., Lee, H.J. and Lee, S.H. 2005. Improvement of nitrogen efficiency by N application at early tillering stage in direct-seeded rice. *Korean J. Crop Sci.*, 50: 16–21.
- SES, IRRI. 2002. Standard Evaluation System. International Rice Research Institute, Manila, Philippines: 11-30.
- Seyed Mostafa, H.M. 2013. Analysis of the relationship between root morphology and uptake of fertilizer nitrogen in rice (*Oryza sativa* L.). *Int. J. Biosciences*, 3(8): 202-209.
- Seyoum, M., Alamerew, S. and Bentte, K. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *J. Plant Sci.*, 7(1): 13-22.
- Shanmugam, A.S. and Rangasamy, S.R.S. 1982. Genetic diversity for quantitative characters in green gram (*Vigna radiata* L.). *The Madras Agri. J.*, 69 (10): 631-636.
- Shantha, N., Tripathi, S., Singh, G.P. and Chaudhary, H.B. 2007. Effect of cultivar and environment on quality characteristics of wheat (*Triticum aestivum* L.). *Indian J. Genet. Plant Breed.*, 67 (2): 149–152.

- Sharma, A. R. and Singh, D. P. 1999. Rice. In: D. L. Smith and C. In: D. L. Smith and C. Hamel (Eds.). Crop yield: Physiology and processes. SpringerVerlag, Berlin. pp. 109-168.
- Sharma, N., Singh, N., Singh, M. and Bharej, T.S. 2008. Quality of aromatic rice in Basmati improvement. Indian J. Agric. Sci., 78(1): 42-49.
- Shellammal, R., Robin, S. and Raveendran, M. 2014. Association and heritability studies for drought resistance under varied moisture stress regimes in backcross inbred population of rice. Rice Sci., 21(3): 150–161.
- Shilpa, J., Bhonsle, and Sellappan, K. 2010. Grain quality evaluation of traditional cultivated rice varieties of Goa, India. Recent Res. Sci. Tech., 2(6): 88-97.
- Shimono, H. and Bunce, J.A. 2009. Acclimation of nitrogen uptake capacity of rice to elevated atmospheric CO₂ concentration. Ann. Botany, 103: 87 – 94.
- Shrivastava, A., Mishra, D.K., Koutu, G.K. and Singh, S.K. 2014. Heritability and genetic advance estimation from parental lines of hybrid rice. Int. J. Sci. Res., 3(7): 11-13.
- Singh, V.N., Singh, A.K., Singh, B.B., Chaturved, G.S., Verma, O.P. and Atlin, G. 2004. In: Poland, D., Sawkins, J., Rabait, M.J. and Hoisinfron, D. Resilient crop for water limited environment: *Proceeding of a workshop*, Cuernavaca Mexico. May 24-28.
- Singh, P. and Singh, V.P. 2007. Quality of direct seeded rice cultivars. Agri. Sci. Digest, 27(2): 79-82.
- Singh, H., Deshmukh, R.K., Singh, A., Singh, A.K., Gaikwad, K., Gaikwad, T., Sharma, T.R., Mohapatra, T. and Singh, N.K. 2009. Highly variable SSR markers suitable for Rice genotyping using Agarose gels. Mol. Breed., 25(2): 359-364.
- Singh, H. and Verma, A. 2013. Characterization and screening of high nitrogen efficient rice genotype to curtail environmental pollution. Int. J. Agri. Environ. Biotech., 6(1): 23-30.

- Singh, V., Jain R.K. and Kumar M. 2013. Genetic analysis of *japonica* × *indica* recombinant inbred lines and characterization of major fragrance gene by microsatellite markers. *Afric. J. Biotech.*, 12(32): 5022-5028.
- Singh, H., Verma, A., Ansari, M.W. and Shukla, A. 2014. Physiological response of rice (*Oryza sativa* L.) genotypes to elevated nitrogen applied under field conditions. *Plant Signaling and Behavior*, 9:e29015; <http://dx.doi.org/10.4161/psb.29015>.
- Soller, M. and Brody, M. 1976. On the power of experimental designs for the detection of linkage between marker loci and quantitative loci in crosses between inbred lines. *Theor. Appl. Genet.*, 47(1): 35-39.
- Srinivasan, S., Gomez, S.M., Kumar, S.S., Ganesh, S.K., Biji, K.R., Senthil, A. and Babu, R.C. 2008. QTLs linked to leaf epicuticular wax, physio-morphological and plant production traits under drought stress in rice (*Oryza sativa* L.). *Plant Growth Regul.*, 56(3) :245-256.
- Srividhya, A., Lakshminarayana R. V., Ramanarao, P.V., Sridhar, S., Jayaprada, M., Anuradha, G., Srilakshmi, B., Reddy, H.K., Hariprasad, A.S., and Siddiq, E.A. 2011. Molecular Mapping of QTLs for Drought Related Traits at Seedling Stage under PEG Induced Stress Conditions in Rice. *American. J. Pl. Sci.*, 2:190-201.
- Steele, K.A., Price, A.H., Witcombe, J.R., Shrestha, R., Singh, B.N., Gibbons, J.M. and Virk, D.S. 2013. QTLs associated with root traits increase yield in upland rice when transferred through marker assisted selection. *Theor. Appl. Genet.*, 126: 101–108.
- Subudhi, H.N., Meher, J., Bose, L.K. and Sanjukta, D. 2009. Genetic diversity studies of promising rice varieties of eastern India based on quality characters. *Oryza*. 46 (3): 224- 227.
- Subudhi, H.N., Swain, D., Das, S., Sharma, S.G. and Singh, O.N. 2012. Studies on grain yield, physico-chemical and cooking characters of elite rice varieties (*Oryza sativa* L.) in Eastern India. *J. Agril. Sci.*, 4(12): 269- 275.

- Suji, K.K., Prince, K.S.J., Mankhar, P.S., Kanagaraj, P., Poornima, R., Amutha, K., Kavitha, S., Biji, K.R., Gomez, S.M., and Babu, C.R. 2012. Evaluation of rice (*Oryza sativa* L.) near iso-genic lines with root QTLs for plant production and root traits in rainfed target populations of environment. *Field Crops Res.*, 137: 89–96.
- Sun, Y.J., Sun, Y.Y., Li, X.Y., Guo, X. and Ma, J. 2009. Relationship of nitrogen utilization and activities of key activities of key enzymes involved in nitrogen metabolism in rice under water–nitrogen interaction, enzymes involved in nitrogen metabolism in rice under water nitrogen interaction. *Acta Agron. Sin.*, 35: 2055-2063.
- Sun, Y., Ma, J., Sun, Y., Xu, H., Yang, Z., Liu, S., Jia, X. and Zheng, H. 2012. The effects of different water and nitrogen managements on yield and nitrogen use efficiency in hybrid rice of China. *Field Crop. Res.*, 127: 8598.
- Swain, D.K., Bhaskar, B.C., Krishnan, P., Rao, K.S., Nayak, S.K. and Dash, R.N. 2006. Variation in yield, N uptake and N use efficiency of medium and late duration rice varieties. *J. Agric. Sci.*, 144: 69-83.
- Tadesse, D., Tadesse, D. and Assefa, A. 2013. Genetic variation in n-use efficiency of malting barley genotypes. *Int. J. Agri. Forestry.* 3(7): 303-308.
- Tanksley, S.D. 1993. Mapping polygenes. *Annu. Rev. Genet.*, 27(1): 205-233.
- Taramino, G. and Tingey, S. 1996. Simple sequence repeats for germplasm analysis and mapping in maize. *Genome*, 39(2): 277-287.
- Tari, D.B., Pirdashti, H.A. and Nasiri, M. 2009. Investigation some agronomical traits of rice under different transplanting dates, planting spaces and nitrogen fertilization in north of Iran. *World Appl. Sci. J.*, 6: 1021–1027.
- Thiem, T.T. and Akira, Y. 2015. Effect of nitrogen application levels on growth of rice under drought stress conditions. *J. Sci. and Devel.*, 13(8): 1388-1396.
- Thoday, J.M. 1961. Location of polygenes. *Nature*, 191(4786): 368-370.
- Thomson, M.J., Septiningsih, Endang, M., Suwardjo, Patimah, Santoso, Tiur, S. and McCouch, S.R. 2007. Genetic diversity analysis of traditional improved

- Indonesian rice (*Oryza sativa* L.) germplasm using microsatellite markers. *Theor. Appl. Genet.*, 114:559-568.
- Tinker, N.A. and Mather, D.E. 1995. MQTL: Software for simplified composite interval mapping of QTL in multiple environments.
- Tong, H.H., Mei, H.W., Yu, X.Q., Xu, X.Y., Li, M.S., Zhang, S.Q and Luo, L.J. 2006. Identification of related QTLs at late developmental stage in rice (*Oryza sativa* L.) under two nitrogen levels. *Acta. Genet. Sin.*, 33(5): 458–467.
- Umadevi, M., Veerabhadhiran, P. and Manonmani, S. 2009. Genetic variability, heritability, genetic advance and correlation for morphological traits in rice genotypes. *Madras Agric. J.*, 96(7-12): 316-318.
- Van Berloo, R. 1999. GGT: software for the display of graphical genotypes. *J. Hered.*, 90: 328-329.
- Vanave, P.B., Apte, U.B., Kadam, S.R. and Thaware, B.L. 2014. Stability analysis for straw and grain yield in rice (*Oryza sativa* L.). *Elec. J. Plant Breed.*, 5(3): 442-444.
- Vanisree, S., Anjali, K., Damodar, R.C., Surender, R.C. and Sreedhar, M. 2013. Variability, heritability and association analysis in scented rice. *J. of Bio. Sci. Opinion*, 1(4): 347-352.
- Venuprasad, V., Shashidhar, H.E. and Hitalmani, S. 2001. QTL Mapping of grain yield and related traits in rice in three diverse environments. *Proceeding of 8th National rice Biotechnology*, 2001, Aurangabad, India. p. 182.
- Venuprasad, R., Shashidhar, H.E., Hitalmani, S. and Hemamalini, G.S. 2002. Tagging quantitative trait loci associated with grain yield and root morphological traits in rice (*Oryza sativa* L.) under contrasting moisture regimes. *Euphytica*, 128 (3): 293-300.
- Venuprasad, R., Dalid, C.O., Del Valle, M., Zhao, D., Espiritu, M., Sta Cruz, M.T., Amante, M., Kumar, A. and Atlin, G.N. 2009. Identification and characterization of large-effect quantitative trait loci for grain yield under lowland drought stress in rice using bulk-segregant analysis. *Theor. Appl. Genet.*, 120(1):177-190.

- Verma, S. 2013. Mapping QTL for root, yield and yield related traits under water stress and non-stress condition using RIL population. Ph. D. thesis. IGKV, Raipur (C.G.).
- Verulkar, S.B., Khillare, A., Raisagar, A., Dudhare, M.S. and Shrivastava, M.N. 2004. Progress in developing drought tolerant rice cultivars for Eastern India. *In: Resilient crop for water limited environment: Proceeding of a workshop held at Cuernavaca Mexico. May 24-28*, pp. 243-244.
- Verulkar, S.B., Mandal, N.P., Dwivedi, J.L., Singh, B.N., Sinha, P.K., Mahato, R.N., Dongre, P., Singh, O.N., Bose, L.K., Swain, P., Robin, S., Babu, R.C., Senthil, S., Jain, A., Shashidhar, H.E., Hittalmani, S., Vara Cruz, C., Paris, T., Raman, A., Haefele, S., Serraj, R., Atlin, G. and Kumar, A. 2010. Breeding resilient and productive genotypes adapted to drought-prone rainfed ecosystem of India. *Field Crop Res.*, 117(2-3): 197-208.
- Wang, B., Lan, T., Wu, W.R. and Li, W.M. 2003. Mapping of QTLs controlling chlorophyll content in rice. *Acta. Genet. Sin.*, 30(12): 1127-1132.
- Wang, Z.Q., Jiang, L., Yi, C.B., Wang, X.L., Lei, J.G., Xiao, Y.L., Liu, X., Liu, S.J., Chen, L.M., Yu, J.Y. and Wan, J.M. 2013. QTL mapping of heterotic loci of yield-related traits in rice. *Chin. J. Rice Sci.*, 27(6): 569–576.
- Wei, D., Cui, K.H., Pan, J.F., Wang, Q., Wang, K., Zhang, X.M., Xiang, J., Nie, L.X. and Huang, J.L. 2011. Identification of quantitative trait loci for grain yield and its components in response to low nitrogen application in rice. *Aust. J. Crop Sci.*, 6(6): 986–994.
- Witcombe, J.R., Hollington, P.A., Howarth, C.J., Reader, S. and Steele, K.A. 2008. Breeding for abiotic stresses for sustainable agriculture. *Phil. Trans. R. Soc. B.*, 363: 703 – 716.
- Wopereis, M.C.S., Kropff, M.J., Maligaya, A.R. and Tuong, T.P. 1996. Drought stress responses of two lowland rice cultivars to soil water status. *Field Crop Res.*, 46(1-3): 21-39.
- Wright, S. 1921. Correlation and causation. *J. Agric. Res.*, 20:257-287.

- Xiao, Y.N., Li, X.H., George, M.L., Li, M.S., Zhang, S.H. and Zheng, Y.L. 2005. Quantitative trait locus analysis of drought tolerance and yield in Maize in China. *Plant Mol. Biol. Rep.*, 23(2): 155-165.
- Xu, Z., Zou, F. and Vision, T. J. 2005. Improving Quantitative Trait Loci mapping resolution in experimental crosses by the use of genotypically selected samples. *Genetics*, 170: 401-408.
- Xu, G., Fan, X. and Miller, A.J. 2012. Plant nitrogen assimilation and use efficiency. *Annu. Rev. Plant Biol.*, 63: 153–82.
- Xu, X., Hea, P., Zhaoa, S., Qiu, S., Johnstond, A. M. and Zhoua, W. 2016. Quantification of yield gap and nutrient use efficiency of irrigated rice in China. *Field Crops Res.*, 186: 58-65.
- Yadav, R., Courtois, B., Huang, N. and McLaren, G. 1997. Mapping genes controlling root morphology and root distribution in a doubled-haploid population of rice. *Theo. Appl. Genet.*, 94:619-632.
- Yamauchi, A., Paradales, J.R., Kono, Y. 1996. Root system structure and its relation to stress tolerance. In: Ito, O., Katayama, K., Johansen, J. V. D. K., Kumar Rao, J. J. (Ed). *Root and nitrogen in cropping systems of the semiarid tropics*, Cultio Corporation, Tsukuba, Japan, : 211–233.
- Yang, G.P., Saghai Maroof, M.A., Xu, C.G., Zhang, Q. and Biyashev, R.M. 1994. Comparative analysis of microsatellite DNA polymorphism in landraces and cultivars of rice. *Mol. Gen. Genet.*, 245(2): 187-194.
- Yang, J., Zhu, J. and Williams, R.W. 2007. Mapping the genetic architecture of complex traits in experimental populations. *Bioinformatics*, 23(12): 1527-1536.
- Yoon, D.B., Kang, K.H., Kim, H.J., Ju, H.G., Kwon, S.J., Suh, J.P., Jeong, O.Y. and Ahn, S.N. 2006. Mapping Quantitative Trait Loci for yield components and morphological traits in an advanced backcross population between *Oryza grandiglumis* and *O. sativa* Japonica Cultivar Hwaseongbyeon. *Theor. Appl. Genet.*, 112:1052- 1062.

- Yu, S.B., Li, J.X., Xu, C.G., Tan, Y.F., Gao, Y.J., Li, X.H., Zhang, Q.F. and Saghai Maroof, M.A. 1997. Importance of epistasis as the genetic basis of heterosis in an elite rice hybrid. *Proceedings of the National Academy of Sciences of the United States of America.*, 94:9226-9231.
- Yue, B., Xue, W., Xiong, L., Yu, X., Luo, L., Cui, K., Jin, D., Xing, Y. and Zhang, Q. 2006. Genetic basis of drought resistance at reproductive stage in rice: separation of drought tolerance from drought avoidance. *Genetics*, 172(2): 1213-1228.
- Zaharath, A.R. and Hanafi, M.M. 2009. Upland rice root characteristics and their relationship to nitrogen uptake. *Pertanika J. Tro. Agri. Sci.*, 32 (2): 261-266.
- Zhang, Y.L., Fan, J.B., Wang, D.S. and Shen, Q.R. 2009. Genotypic differences in grain yield and physiological nitrogen use efficiency among rice cultivars. *Pedosphere*, 19(6): 681–691.
- Zhong-cheng, L., Qi-gen, D., Shi-chao, Y., Fu-guan, W., Yu-shu, J., Jing-dou, C., Lu-sheng, X., Hong-cheng, Z., Zhong-yang, H., Ke, X. and Hai-yan, W. 2012. Effects of nitrogen application level on ammonia volatilization and nitrogen utilization during the rice growing season. *Rice Sci.*, 19(2):125-134.
- Zhu, G., Peng, S., Huang, J., Cui, k., Nie, L. and Wang, F. 2016. Genetic improvements in rice yield and concomitant increases in radiation- and nitrogen-use efficiency in middle reaches of yangtze river. *Scientific Reports*, 6:21049. DOI: 10.1038/srep21049.
- Zou, C., Shen, J., Zhang, F., Guo, S., Rengel, Z. and Tang, C. 2001. Impact of nitrogen form on iron uptake and distribution in maize seedlings in solution culture. *Plant Soil*, 235: 143–149.
- Zou, G.H., Mei, H.W., Liu, H.Y., Liu, G.L., Hu, S.P. and Yu, X.Q. 2005. Grain yield responses to moisture regimes in a rice population: association among traits and genetic markers. *Theor. Appl. Genet.*, 112: 106–113.

Appendix (A): Standard meteorological week's average weather data during the crop growth period (June 18, 2015 – Nov. 11, 2015)

Wk No.	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rainfall (mm)	Rainy days	Relative Humidity (%)		Vapour Pressure (mm of Hg)		Wind Velocity (Kmph)	Evaporation (mm)	Sun Shine (hours)
						I	II	I	II			
25	Jun 18-24	33.8	25.8	201.8	3	85.0	72.0	23.3	22.4	7.9	5.3	4.9
26	25-01	33.5	25.0	25.8	4	87.0	59.0	22.8	21.6	9.3	6.4	4.3
27	Jul 02-08	33.6	25.2	41.8	2	79.0	64.0	21.7	22.0	9.1	6.4	5.9
28	09-15	31.2	25.2	72.8	5	89.0	80.0	23.2	24.1	7.9	3.3	1.7
29	16-22	31.8	25.6	7.8	1	91.0	71.0	23.4	23.6	8.0	4.7	2.4
30	23-29	30.7	25.1	43.6	1	90.0	70.0	22.3	21.6	7.9	4.1	3.4
31	30-05	31.2	25.2	48.7	3	86.0	69.0	21.3	21.2	10.4	4.6	4.6
32	Aug 06-12	30.8	24.7	36.6	1	94.0	73.0	23.2	23.7	4.8	3.1	2.5
33	13-19	31.7	25.3	126.4	3	94.0	73.0	24.0	24.2	7.5	4.7	4.1
34	20-26	32.3	25.9	23.6	1	87.0	65.0	22.6	22.0	8.1	5.0	6.5
35	27-02	30.8	25.0	37.9	6	94.0	80.0	23.5	24.7	4.9	2.5	1.2
36	Sep 03-09	33.0	25.5	10.0	1	93.0	64.0	23.7	21.5	4.7	3.9	6.9
37	10-16	33.5	25.4	68.4	2	93.0	62.0	23.9	22.0	3.8	4.7	6.8
38	17-23	30.1	25.1	135.4	2	94.0	78.0	23.6	24.0	5.8	2.6	3.1
39	24-30	32.5	24.6	0.0	0	92.0	57.0	22.3	20.2	3.0	3.8	7.2
40	Oct 01-07	33.7	24.4	0.0	0	92.0	51.0	22.7	19.3	2.4	4.4	7.7
41	08-14	33.9	22.2	0.0	0	89.0	47.0	19.5	17.9	3.0	4.3	8.7
42	15-21	33.4	22.8	0.0	0	91.0	45.0	20.2	16.7	2.4	3.8	8.7
43	22-28	33.7	21.3	0.0	0	90.0	37.0	18.5	13.8	2.1	3.6	8.2
44	29-04	30.0	19.4	0.0	0	90.0	55.0	16.6	16.4	4.1	3.2	6.7
45	Nov 05-11	31.7	18.8	0.0	0	91.0	37.0	15.8	12.4	2.6	3.5	7.8

Appendix (B): Standard meteorological week's average weather data during the crop growth period (June 19, 2016 – Nov. 12, 2016)

Wk. No.	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rainfall (mm)	Rainy days	Relative Humidity (%)		Vapour Pressure (mm of Hg)		Wind Velocity (Kmph)	Evaporation (mm)	Sun Shine (hours)
						I	II	I	II			
26	June 19-25	34.7	26.5	29.8	3	84.8	54.4	23.3	21.5	5.2	5.6	5.2
27	26-02	34.8	26.2	32.4	3	88.2	60.0	23.7	23.4	6.	6.1	7.5
28	July 03-09	29.2	24.5	114.8	6	96.4	86.2	22.9	24.0	11.0	3.2	0.7
29	10-16	30.4	24.6	122.0	5	91.5	80.0	22.5	22.9	7.9	3.5	1.9
30	17-23	30.2	24.8	145.6	5	93.1	77.8	23.1	23.8	5.4	2.9	1.2
31	24-30	32.0	25.3	53.6	4	91.4	67.5	23.5	23.1	4.2	5.0	5.9
32	31-06	25.9	25.2	85.6	4	92.7	86.1	23.0	24.0	7.3	2.5	2.0
33	Aug 07-13	29.3	22.1	51.8	3	89.2	73.5	21.9	22.2	8.9	9.0	2.1
34	14-20	28.7	21.4	11.6	3	88.2	74.1	21.4	21.1	8.9	2.6	2.0
35	21-27	31.7	25.6	26.4	2	92.0	72.2	23.6	22.8	4.4	3.9	4.1
36	28-03	32.5	25.9	53.8	1	90.0	66.8	24.3	23.5	4.3	3.7	4.9
37	Sep 04-10	30.5	25.2	44.6	2	86.2	68.5	21.8	21.9	5.0	3.2	1.1
38	11-17	31.0	24.6	97.2	4	94.2	78.7	23.5	24.1	2.8	3.6	3.9
39	18-24	32.2	24.7	91.6	3	94.4	69.4	23.8	23.4	3.0	4.7	6.2
40	25-01	29.5	24.4	146.2	7	97.0	88.1	23.5	23.9	2.4	3.1	3.0
41	Oct 02-08	30.7	24.6	45.0	5	96.2	72.7	23.7	23.2	2.3	3.1	4.0
42	09-15	31.9	22.3	0.8	0	92.0	42.5	19.8	14.9	1.3	3.6	6.7
43	16-22	31.3	18.7	0.0	0	91.1	35.8	16.3	12.0	1.1	3.9	10.1
44	23-29	31.4	18.4	0.0	0	86.5	39.1	14.8	13.0	1.6	3.7	9.2
45	30-05	30.5	19.8	0.0	0	85.1	49.1	15.6	15.4	2.2	3.4	8.1
46	Nov 06-12	29.9	14.4	0.0	0	89.0	26.7	11.9	8.1	1.6	3.4	8.4

Appendix (C): Scoring of 38 germplasm accessions.

Marker	Band size	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
RM-431	250	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0
	255	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1
	160	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
RM-154	170	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0
	175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
	180	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1
RM-233	185	0	0	0	0	0	1	1	1	1	1	0	1	0	0	0	0	0	0	0
	145	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	150	0	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
RM-55	160	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
	170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	230	1	1	1	1	1	1	1	1	0	0	NA	0	0	0	NA	0	0	0	0
RM-307	250	0	0	0	0	0	0	0	0	1	1	NA	1	1	1	NA	1	1	1	1
	210	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	250	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-161	160	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	175	0	0	0	1	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0
	125	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-162	180	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	275	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	120	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-454	125	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	150	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	155	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-455	125	1	1	1	1	1	NA	1	1	0	0	0	0	0	0	0	0	0	0	0
	130	0	0	0	0	0	NA	0	0	1	1	1	1	1	1	1	1	1	1	1
	135	0	0	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-44	600	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	125	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	130	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-408	200	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	220	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	225	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-316	125	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	200	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	400	1	0	0	0	NA	0	1	0	0	0	1	1	1	1	0	1	0	0	0
HvSSR-10-01	500	0	1	1	1	NA	1	0	1	1	1	0	0	0	0	1	0	1	1	1
	325	1	1	0	0	0	0	1	0	NA	0	1	1	1	1	0	0	0	0	0
	400	0	0	1	0	1	0	0	0	NA	1	0	0	0	0	0	0	1	0	0
RM-144	500	0	0	0	1	0	1	0	1	NA	0	0	0	0	0	1	1	0	1	1
	225	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	250	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-536	300	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	310	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	150	0	0	NA	1	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0
RM-1233	155	1	1	NA	0	1	1	NA	0	1	1	0	0	1	1	0	1	0	0	0
	160	0	0	NA	0	0	0	NA	1	0	0	1	1	0	0	1	0	0	0	0
	165	0	0	NA	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	0	0
RM-277	170	0	0	NA	0	0	0	NA	0	0	0	0	0	0	0	0	0	0	1	1
	175	0	0	NA	0	0	0	NA	0	0	0	0	0	0	0	0	0	1	0	0
	120	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
RM-1261	125	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	205	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	210	1	0	1	0	0	0	1	1	1	1	1	1	1	1	0	1	0	1	1
RM-1261	215	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
	240	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
	250	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

Appendix- C continued...

Marker	Band size	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38
RM-431	250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	255	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	160	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	170	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-154	175	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	180	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
	185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	145	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-233	150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	160	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	170	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	230	0	0	0	0	0	0	0	0	0	0	NA	NA	NA	NA	NA	NA	NA	NA	NA
RM-55	250	1	1	1	1	1	1	1	1	1	1	NA	NA	NA	NA	NA	NA	NA	NA	NA
	RM-307	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	RM-161	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-162	175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	125	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	160	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	275	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-454	RM-588	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	125	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	155	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-455	125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	135	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	600	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-44	125	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1
	130	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	200	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	RM-242	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-316	225	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0
	125	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	200	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
	HvSSR-10-01	400	0	1	1	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0
HvSSR-10-17	500	1	1	0	0	1	0	0	0	0	0	0	0	1	1	NA	1	1	0	0
	325	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	400	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	500	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	0	0
RM-144	225	0	1	0	1	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0
	250	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	300	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	0	0	0
	310	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-1233	150	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	155	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	160	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-277	170	1	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
	175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	120	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	125	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RM-1261	205	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	210	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	215	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	240	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RM-1261	250	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

Appendix (D): Scoring of RILs population

Marker	Swarna	Basmati-370	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
RM-302	0	1	1	0	NA	0	0	0	1	1	0	0	1	NA	0	1	1	0
RM-6504	0	1	0	0	0	1	1	1	1	1	0	0	1	0	0	0	0	0
RM-12146	0	1	1	1	0	1	1	1	1	1	0	0	0	1	1	1	0	1
RM-163	0	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1
RM-18615	0	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1
RM-18616	0	1	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0
RM-18620	0	1	1	1	0	1	0	0	0	1	0	0	0	0	1	1	0	0
RM-18655	0	1	0	0	0	1	0	0	0	1	NA	0	0	0	0	0	0	0
RM-408	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
RM-22565	0	1	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0
RM-22710	0	1	1	NA	1	1	1	1	1	1	0	NA	0	1	NA	1	1	1
RM-24568	0	1	1	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0
RM-24571	0	1	1	0	NA	0	0	0	0	1	0	0	0	0	0	0	0	0
HvSSR 9-37	0	1	1	0	0	0	0	0	0	1	0	0	0	0	1	1	1	0
RM-1233	0	1	1	1	1	1	1	1	1	0	1	1	0	0	1	1	0	0
RM-1261	0	1	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0
RM-7195	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0

0- Swarna type, 1- Basmati-370 type and NA- Not amplified

Appendix (E): Adjusted mean of 85 germplasm accessions with 7 checks of eleven yield traits for N⁰ under aerobic condition during wet season-2015

Sr. No.	Entry	Adjusted mean										
		DF	PHSD	CCSD	CCFW	PHMT	PL	SPP	FGP	SF	TW	GY
1	RP 5125-2-4	89.7	26.3	34.9	36.8	97.0	22.9	115.0	102.0	87.4	2.1	217.9
2	R 1779-321-1-112-1	88.7	24.7	38.3	34.4	76.0	21.3	118.6	105.2	87.5	1.7	122.9
3	R 1882-306-4-243-1	87.7	24.8	36.3	32.8	86.2	21.5	103.8	89.2	84.4	1.5	195.4
4	R 1892-486-1-151-1	90.7	27.2	32.6	35.8	68.3	20.3	83.2	68.4	80.1	2.0	96.6
5	BP 10620 F-BB 4-13-BB 8	89.7	26.2	32.1	31.1	73.0	20.8	64.0	50.8	76.4	2.0	165.4
6	R 1674-1823-2-1189-1	96.7	28.9	31.5	34.8	77.5	20.9	81.8	47.6	57.1	1.5	71.6
7	R 1973-206-2-86-1	92.7	28.1	29.0	34.8	68.2	19.3	86.6	64.0	72.3	1.5	126.6
8	R 2093-1536-1-660-1	86.7	28.6	29.1	26.9	66.4	21.8	73.4	62.2	82.1	1.7	117.9
9	IR 84887-B-15	84.7	32.1	30.9	31.7	81.2	21.1	118.2	93.0	77.8	1.8	127.9
10	R 1700-308-3-170-1	90.7	25.6	28.3	35.3	66.8	21.2	100.0	85.2	83.6	1.7	152.9
11	IR 83376-B-B-110-3	86.7	30.5	28.4	27.4	70.8	18.4	93.4	73.2	76.8	1.6	190.4
12	R 1917-951-1-541-1	88.7	31.4	25.9	31.5	71.4	21.2	99.6	89.2	87.8	1.8	117.9
13	R 1700-309-1-171-1	87.7	26.8	29.8	32.1	70.6	19.3	97.0	89.4	90.2	1.9	157.9
14	R 1672-1171-1-124-1	89.7	26.8	34.2	32.7	67.1	20.5	81.8	68.4	81.4	1.7	81.6
15	R 1695-133-1-72-1	89.7	24.8	28.7	34.7	69.2	19.7	79.2	63.8	78.4	2.2	96.6
16	R 1262-1667-1-1	92.0	22.6	29.6	35.2	72.2	20.4	145.5	93.4	65.1	2.2	149.1
17	R 1860-783-1-424-1	87.0	22.5	34.3	37.1	83.9	22.3	147.7	125.6	84.5	1.9	174.1
18	R 1670-3269-2-3926-1	89.0	23.9	32.8	41.5	83.2	22.3	99.5	76.6	77.1	1.7	116.6
19	BRR-0006	92.0	27.9	32.3	32.9	89.9	25.2	103.3	83.6	80.7	1.8	141.6
20	RAU 1484-Aer-04	91.0	27.2	30.7	34.7	94.4	23.1	176.1	101.6	58.8	1.8	142.9
21	RCPR 8	88.0	27.6	29.9	35.4	98.0	24.6	141.5	111.6	78.8	2.1	216.6
22	RCPR 6	89.0	30.4	30.0	30.9	95.6	23.1	112.1	78.4	70.6	1.9	144.1
23	BRR-0007	91.0	29.6	35.3	37.0	82.4	24.4	181.7	91.6	51.8	1.6	136.6
24	R 1240-913-2-1013-1	101.0	24.3	31.2	35.8	88.2	20.8	81.7	59.8	73.8	1.6	61.6
25	CR-3631-1-3	91.0	26.6	29.7	31.0	97.1	22.9	145.9	132.2	89.7	1.9	282.9
26	CB 09 512	89.0	29.0	35.1	37.8	84.2	22.2	120.3	74.2	63.0	1.9	212.9
27	CR 3632-1-2	90.0	25.7	34.0	34.3	82.2	19.1	111.5	92.8	82.8	1.9	216.6
28	CR 3634-1-3	89.0	25.9	30.9	31.6	84.6	21.7	126.3	111.2	87.2	2.0	186.6
29	Anjali	72.0	23.0	35.4	29.0	87.4	24.9	93.7	78.0	82.7	2.1	131.6
30	Neha	71.0	27.6	32.4	27.1	50.8	17.3	25.9	14.6	63.0	1.6	66.6
31	CR Dhan 40	75.0	31.4	33.7	28.9	99.8	23.2	171.9	118.8	69.5	1.8	276.6
32	Poornima	82.0	21.9	30.0	27.9	73.0	19.7	96.5	80.6	83.0	2.0	135.4
33	R 2212-RF-75	81.3	21.4	37.7	43.7	80.9	21.4	134.1	98.7	73.2	2.1	149.1
34	R 1033-968-2-1	87.3	24.6	40.0	41.0	75.3	19.8	112.5	97.7	87.8	2.2	220.4
35	R 1744-4901-1-1-510-1	92.3	17.3	36.4	27.3	75.1	19.4	83.7	61.3	73.4	2.0	102.9

36	R-RHZ-2	82.3	24.4	39.4	31.8	82.9	21.2	151.1	133.7	89.0	1.8	247.9
37	R-RF 105	89.3	22.4	34.6	33.8	85.8	22.9	138.9	123.9	89.9	1.7	271.6
38	R 1670-3269-2-3926-1	90.3	21.1	34.0	39.6	71.8	20.9	149.1	124.7	83.8	1.4	265.4
39	R 1678-1901-1-1473-1	93.3	22.5	33.3	40.3	78.9	21.9	124.1	99.7	80.6	1.7	190.4
40	R 1902-912-2-512-1	92.3	21.8	37.8	37.3	75.7	21.2	136.9	109.5	80.1	1.5	234.1
41	R 1695-270-2-133-1	89.3	20.8	37.5	32.9	71.4	21.7	109.1	89.3	82.4	2.3	209.1
42	MTU 1010	92.3	22.3	33.6	37.9	61.8	18.7	78.5	64.7	83.8	2.2	142.9
43	R 1598-483-1-297-1	95.3	24.1	32.2	36.4	70.8	20.5	81.7	71.9	90.0	2.1	199.1
44	R 1570-2649-1-1546-1	93.3	17.7	33.5	38.1	76.4	22.6	182.7	140.9	76.7	1.6	220.4
45	R 1670-3975-1-485-1	94.3	19.5	33.5	37.5	69.0	22.4	62.5	46.9	76.0	1.9	185.4
46	R 1570-2644-2-1547-1	93.3	22.0	33.8	33.5	78.6	23.5	185.3	131.1	70.0	1.5	302.9
47	IGKVR 1	98.3	19.3	34.7	38.9	73.7	20.4	174.1	107.7	60.7	2.4	99.1
48	R 1702-3677-1-4734-1	92.3	21.3	34.1	39.2	62.6	21.5	115.3	70.1	59.5	1.7	109.1
49	R 741-1-55-2-1-R-1	105.3	26.2	34.2	37.9	82.9	22.0	82.3	56.9	68.8	1.8	52.9
50	Chandrasahini	93.3	24.5	36.6	38.3	68.7	21.7	155.1	111.7	71.4	2.2	167.9
51	R-RHZ-LI-22	106.3	30.4	36.4	37.8	82.2	20.9	84.3	55.9	65.6	2.0	41.6
52	R 1432-251-103-1-1	91.3	22.5	33.1	31.8	76.8	21.4	176.1	123.7	69.5	1.9	244.1
53	IGKVR 1244	102.3	20.1	34.4	40.2	73.1	20.5	128.1	100.1	78.2	2.2	96.6
54	Mahamaya	94.3	21.1	32.9	42.4	74.3	19.0	126.1	103.9	82.8	2.0	81.6
55	R 1700-2243-2-2312-1	92.3	21.5	34.4	38.6	72.2	22.5	104.0	83.0	80.5	1.7	116.1
56	R 1641-914-1-400-1	104.3	19.8	33.7	37.9	73.8	21.8	81.2	53.2	65.5	1.4	21.1
57	IGKVR 2	92.3	25.8	34.7	42.4	83.7	19.4	165.8	89.2	53.2	1.7	103.6
58	R 1747-4941-1-515-1	92.3	22.9	28.3	31.6	77.5	20.9	133.0	106.6	80.6	1.9	139.9
59	CGR-547 (Bargi)	78.3	30.2	27.3	31.2	108.1	21.2	147.2	107.2	72.9	2.2	158.6
60	Anjan I	97.3	22.8	28.8	31.8	120.6	24.1	74.6	52.2	70.3	1.3	54.9
61	Badshah Bhog II	94.3	33.7	28.0	28.9	116.4	21.0	112.6	66.2	58.3	1.9	41.1
62	Jogi Bhog	93.3	29.7	30.6	34.2	130.8	23.0	82.4	52.8	63.9	1.9	94.9
63	Anjan II	96.3	30.8	31.0	34.4	117.1	23.5	145.2	96.8	66.5	1.6	158.6
64	Anjan	95.3	29.2	31.0	39.3	119.9	24.4	197.8	90.2	44.9	1.3	104.9
65	Lal Banko	88.8	28.0	27.8	33.0	99.4	19.7	95.3	77.1	81.7	2.0	96.5
66	Mudi Banko	98.8	31.7	29.5	28.1	117.6	22.9	145.5	87.3	60.5	1.7	126.5
67	Raj Banko	94.8	30.0	29.5	32.0	121.3	19.9	150.9	81.3	54.4	1.9	120.2
68	Byarangi	101.8	28.6	27.9	33.1	83.0	21.7	156.7	91.1	58.7	1.7	97.7
69	Barangi	100.8	35.0	27.4	27.8	100.5	20.7	140.5	91.9	66.0	1.5	120.2
70	Mauhakuchi	99.8	31.2	25.0	28.5	103.8	19.3	97.9	59.3	61.3	1.7	142.7
71	Rajpiti (A)	100.8	31.5	34.3	31.3	106.3	20.6	77.7	55.1	71.8	1.6	106.5
72	Digamber Dhan	81.8	27.9	33.8	34.4	83.7	19.1	151.9	121.3	80.4	1.6	356.5
73	Dadhmaini Dhan	87.8	29.4	34.8	32.8	78.5	19.1	122.1	105.5	87.0	1.5	324.0
74	Chhota Dhan	94.8	33.5	31.7	36.6	101.0	22.4	81.9	58.3	72.1	1.9	142.7
75	Safed Lalak	85.8	27.2	31.5	37.8	74.6	20.3	104.1	89.7	86.9	1.9	250.2
76	Sitasaal Dhan	86.8	28.7	31.8	28.4	72.9	21.4	74.1	60.7	82.9	1.8	265.2

Appendix (F): Adjusted mean of 85 germplasm accessions with 7 checks of eleven yield traits for NO₃-N under aerobic condition during wet season-2015

Sr. No.	Entry	Adjusted mean										
		DF	PHSD	CCSD	CCFW	PHMT	PL	SPP	FGP	SF	TW	GY
1	RP 5125-2-4	86.8	31.3	40.3	40.1	106.8	24.3	140.7	126.2	89.5	2.3	347.5
2	R 1779-321-1-112-1	87.8	27.5	41.3	42.2	85.1	23.1	136.7	122.2	89.1	1.9	268.7
3	R 1882-306-4-243-1	88.8	24.1	39.1	37.7	87.0	22.2	106.5	96.8	89.9	2.1	208.7
4	R 1892-486-1-151-1	89.8	30.7	36.4	39.8	74.4	19.8	69.5	61.4	85.9	2.6	118.7
5	BP 10620 F-BB 4-13-BB 8	90.8	27.3	36.6	37.4	72.3	19.9	107.5	85.4	78.8	2.4	228.7
6	R 1674-1823-2-1189-1	97.8	26.9	35.7	38.3	77.3	21.7	131.9	83.2	63.2	1.9	80.0
7	R 1973-206-2-86-1	90.8	25.7	35.0	37.1	73.3	20.8	96.5	77.0	78.8	1.9	203.7
8	R 2093-1536-1-660-1	84.8	29.9	35.9	37.9	87.6	24.1	122.7	103.2	83.7	2.0	272.5
9	IR 84887-B-15	85.8	31.3	34.8	36.5	90.7	22.7	139.7	123.2	88.0	2.0	292.5
10	R 1700-308-3-170-1	91.8	25.4	33.9	40.0	67.5	21.3	121.7	100.2	81.9	1.9	162.5
11	IR 83376-B-B-110-3	86.8	29.9	30.9	33.5	78.6	18.5	100.7	88.2	86.5	2.3	182.5
12	R 1917-951-1-541-1	86.8	28.9	33.8	37.1	70.2	21.2	112.7	99.2	87.3	2.7	228.7
13	R 1700-309-1-171-1	89.8	28.1	32.6	36.7	76.9	21.1	148.7	139.2	93.5	2.5	267.5
14	R 1672-1171-1-124-1	89.8	27.5	36.6	39.8	82.7	24.5	110.5	85.6	76.9	1.8	228.7
15	R 1695-1133-1-72-1	86.8	25.6	34.7	39.7	78.1	22.2	111.7	93.4	83.0	2.3	172.5
16	R 1262-1667-1-1	89.9	21.7	33.0	39.6	77.0	20.9	149.6	121.9	81.8	2.3	241.8
17	R 1860-783-1-424-1	87.9	22.4	38.8	39.3	87.1	22.0	143.2	111.5	78.2	2.1	304.3
18	R 1670-3269-2-3926-1	88.9	22.9	30.0	40.4	75.4	20.9	162.4	112.7	69.5	1.9	215.5
19	BRR-0006	89.9	30.6	33.6	39.8	93.8	25.7	118.6	85.9	73.2	1.2	215.5
20	RAU 1484-Aer-04	89.9	27.8	34.0	38.0	99.3	23.0	161.0	135.9	84.5	2.3	271.8
21	RCPR 8	89.9	28.8	33.6	37.8	100.5	24.2	172.2	138.5	80.5	2.1	309.3
22	RCPR 6	88.9	27.1	33.1	34.4	99.5	24.3	131.2	104.5	80.2	2.2	253.0
23	BRR-0007	91.9	31.3	34.6	39.4	89.2	24.4	167.6	109.9	65.7	2.1	204.3
24	R 1240-913-2-1013-1	101.9	25.8	36.9	33.6	98.9	21.5	104.4	70.5	68.6	1.7	46.8
25	CR-3631-1-3	87.9	25.9	36.8	37.0	95.3	21.2	122.4	101.7	83.8	2.3	244.3
26	CB 09 512	89.9	29.6	37.3	39.1	89.1	20.0	121.6	76.1	63.3	1.9	228.0
27	CR 3632-1-2	89.9	27.6	37.5	37.2	90.6	21.7	131.6	115.9	88.6	2.0	236.8
28	CR 3634-1-3	87.9	28.6	32.2	35.0	88.5	22.9	141.6	114.9	81.5	2.2	190.5
29	Anjali	68.9	23.8	35.7	37.1	79.5	22.2	114.6	93.9	82.8	2.5	170.5
30	Neha	68.9	27.1	31.6	36.8	51.5	17.5	62.2	49.5	82.4	2.0	49.3
31	CR Dhan 40	75.9	31.3	34.3	31.9	106.3	24.8	164.2	134.1	81.8	1.9	280.5
32	Poomima	77.9	22.9	33.2	36.4	76.7	20.1	122.8	93.9	77.2	2.4	186.8
33	R 2212-RF-75	81.2	28.8	41.9	41.3	86.3	22.1	148.8	108.0	72.8	2.3	216.9
34	R 1033-968-2-1	88.2	26.2	38.7	43.4	84.7	19.3	90.2	69.0	75.7	2.2	210.7
35	R 1744-4901-1-1-510-1	91.2	22.3	38.2	38.5	81.2	19.8	110.0	89.4	80.8	2.2	139.4
36	R-RHZ-2	83.2	27.1	41.9	40.2	90.8	20.6	166.0	132.8	80.3	2.3	361.9

37	R-RF 105	88.2	25.5	40.1	40.8	102.6	24.5	135.8	124.0	91.1	2.4	339.4
38	R 1670-3269-2-3926-1	92.2	27.1	37.9	41.2	89.6	22.6	120.6	103.8	85.7	1.9	214.4
39	R 1678-1901-1-1473-1	94.2	25.2	40.1	43.2	82.6	23.4	117.8	104.0	87.8	2.2	215.7
40	R 1902-912-2-512-1	91.2	25.0	38.5	42.2	83.2	21.3	146.8	119.6	81.5	2.1	206.9
41	R 1695-270-2-133-1	89.2	25.0	39.3	43.6	81.7	23.3	93.6	58.4	61.9	1.9	185.7
42	MTU 1010	93.2	25.9	36.8	40.6	78.2	20.8	70.8	61.0	84.4	2.3	188.2
43	R 1598-483-1-297-1	95.2	26.7	38.4	40.2	73.0	19.7	78.0	63.8	80.4	2.1	155.7
44	R 1570-2649-1-1546-1	93.2	23.2	37.2	37.3	76.4	21.9	101.2	62.4	61.4	1.5	150.7
45	R 1670-3975-1-485-1	95.2	23.3	37.2	44.6	77.6	23.6	113.4	77.2	67.9	1.8	180.7
46	R 1570-2644-2-1547-1	93.2	24.2	39.5	35.9	86.7	23.3	166.0	119.8	72.5	1.6	260.7
47	IGKVR 1	100.2	26.3	40.9	37.8	78.8	20.6	130.2	87.2	67.0	2.0	66.9
48	R 1702-3677-1-4734-1	94.2	24.8	41.8	43.8	79.2	24.6	83.6	56.0	66.2	1.8	129.4
49	R 741-1-55-2-1-R-1	102.2	28.5	38.4	38.9	95.1	22.9	82.6	61.0	72.8	1.8	84.4
50	Chandrasini	94.2	25.3	37.0	33.1	76.3	23.2	108.6	73.8	67.7	2.0	125.7
51	R-RHZ-LI-22	108.2	29.0	39.7	43.4	92.6	21.4	77.4	58.2	74.0	2.0	79.4
52	R 1432-251-103-1-1	91.2	26.2	38.1	35.6	82.3	21.5	154.0	121.8	79.2	1.8	240.7
53	IGKVR 1244	100.2	28.0	41.6	35.8	77.8	21.4	60.6	45.2	72.6	2.5	96.9
54	Mahamaya	100.2	25.2	39.3	40.9	81.1	19.3	113.4	85.2	74.8	2.6	91.9
55	R 1700-2243-2-2312-1	94.8	24.1	34.4	39.1	65.1	23.9	123.7	74.2	58.9	2.1	114.1
56	R 1641-914-1-400-1	106.8	22.6	34.6	38.5	72.6	22.6	81.5	59.2	72.4	2.3	51.6
57	IGKVR 2	94.8	25.0	38.2	41.6	85.0	19.9	100.7	74.0	73.2	2.2	105.3
58	R 1747-4941-1-515-1	89.8	26.3	35.6	37.5	78.6	21.1	105.3	84.4	80.2	2.6	114.1
59	CGR-547 (Bargi)	79.8	33.4	29.7	37.1	116.2	23.5	141.9	116.4	81.9	2.6	265.3
60	Anjan I	99.8	29.8	30.7	33.1	120.0	24.1	80.7	56.6	69.7	1.6	61.6
61	Badshah Bhog II	94.8	30.4	29.7	30.8	126.7	21.2	141.3	83.4	57.9	2.3	95.3
62	Jogi Bhog	93.8	33.7	30.0	38.6	129.9	23.3	93.7	59.2	62.2	2.1	67.8
63	Anjan II	94.8	28.6	31.3	36.6	124.8	24.3	144.3	84.8	57.6	2.2	206.6
64	Anjan	95.8	28.7	31.5	34.7	124.6	26.5	149.9	101.4	66.9	2.0	51.6
65	Lal Banko	89.2	32.6	34.5	38.7	124.9	24.8	73.8	60.3	82.7	2.1	84.8
66	Mudi Banko	102.2	30.6	32.1	30.2	123.2	24.9	85.6	63.1	74.5	1.8	87.3
67	Raj Banko	94.2	32.5	38.1	36.8	123.1	22.1	88.4	72.7	82.9	2.3	126.0
68	Byarangi	99.2	31.4	31.7	33.7	112.8	24.5	107.6	74.1	69.3	2.2	121.0
69	Barangi	99.2	35.0	35.3	33.5	88.6	23.9	125.4	93.9	75.0	2.1	99.8
70	Maubakuchi	99.2	30.9	31.7	31.6	112.8	22.4	114.0	70.9	62.6	2.1	88.5
71	Rajjiti (A)	102.2	31.4	36.3	38.4	117.8	24.2	109.0	47.3	44.0	1.9	53.5
72	Digamber Dhan	86.2	30.8	34.6	38.7	99.6	21.0	143.0	114.7	80.1	2.1	299.8
73	Dadhmaini Dhan	89.2	30.8	36.4	41.0	95.3	22.2	131.0	99.5	76.0	2.1	267.3
74	Chhota Dhan	98.2	33.4	33.4	38.7	105.2	22.9	99.4	70.9	71.9	2.1	152.3
75	Safed Lalak	86.2	28.5	29.9	37.3	80.4	21.3	120.0	86.5	72.3	2.3	228.5
76	Sitasaal Dhan	85.2	26.3	34.9	38.3	78.6	21.5	72.8	54.9	76.5	2.5	188.5
77	Tewan Dhan	99.2	26.3	34.4	35.4	77.0	19.7	63.6	43.7	70.3	1.9	117.3

Appendix (G): Adjusted mean of 85 germplasm accessions with 7 checks of eleven yield traits for NH_4N under aerobic condition during wet season-2015

Sr. No.	Entry	Adjusted mean										
		DF	PHSD	CCSD	CCFW	PHMT	PL	SPP	FGP	SF	TW	GY
1	RP 5125-2-4	88.4	33.4	41.5	42.4	124.8	26.2	133.1	104.3	78.1	2.4	205.5
2	R 1779-321-1-112-1	86.4	29.5	37.9	41.4	101.7	25.1	126.5	99.3	78.3	2.2	208.0
3	R 1882-306-4-243-1	87.4	25.4	40.1	41.6	105.1	26.3	146.5	127.3	86.4	2.1	285.5
4	R 1892-486-1-151-1	90.4	28.3	40.4	41.3	93.7	22.0	110.1	68.7	62.8	2.6	98.0
5	BP 10620 F-BB 4-13-BB 8	91.4	24.3	42.8	40.0	87.5	20.8	118.5	89.7	75.6	2.6	221.8
6	R 1674-1823-2-1189-1	91.4	25.3	38.6	40.1	89.7	22.3	141.1	99.5	70.4	2.0	91.8
7	R 1973-206-2-86-1	93.4	28.9	35.7	41.0	94.8	23.0	81.3	57.1	70.8	1.9	200.5
8	R 2093-1536-1-660-1	85.4	29.2	40.8	40.6	93.7	21.5	134.5	109.3	80.9	2.1	226.8
9	IR 84887-B-15	87.4	33.7	37.5	37.4	114.2	27.8	134.5	114.3	84.6	2.0	270.5
10	R 1700-308-3-170-1	92.4	23.4	37.7	44.0	81.6	22.5	130.5	81.5	62.6	1.9	158.0
11	IR 83376-B-B-110-3	87.4	31.3	37.2	37.4	90.2	22.1	131.5	105.3	79.8	2.1	301.8
12	R 1917-951-1-541-1	89.4	26.6	36.8	38.4	96.5	24.6	137.5	102.3	74.2	2.3	229.3
13	R 1700-309-1-171-1	89.4	32.5	38.4	38.0	85.6	22.0	102.5	92.3	89.6	2.2	186.8
14	R 1672-1171-1-124-1	91.4	30.4	38.2	37.5	86.3	23.9	131.1	99.3	75.6	2.1	300.5
15	R 1695-133-1-72-1	85.4	23.9	33.3	39.3	86.5	22.5	129.9	103.3	79.3	2.5	248.0
16	R 1262-1667-1-1	92.4	21.8	34.8	44.8	82.1	24.5	137.3	118.8	86.0	1.9	305.7
17	R 1860-783-1-424-1	89.4	23.2	39.6	41.8	99.2	24.1	164.3	150.8	91.2	2.0	323.2
18	R 1670-3269-2-3926-1	88.4	23.7	36.7	39.7	92.3	24.7	149.1	128.4	85.7	1.9	280.7
19	BRR-0006	92.4	35.2	41.6	39.1	97.9	25.9	118.3	98.8	82.9	2.0	234.5
20	RAU 1484-Aer-04	91.4	31.9	38.3	39.8	99.3	22.7	139.7	118.2	84.2	2.1	235.7
21	RCPR 8	92.4	31.6	38.7	41.0	104.5	24.1	155.3	144.8	92.5	2.3	314.5
22	RCPR 6	90.4	25.4	34.0	41.4	103.7	24.7	119.9	98.8	81.8	2.1	300.7
23	BRR-0007	93.4	29.3	38.5	40.3	91.7	27.1	168.3	91.8	55.7	2.0	158.2
24	R 1240-913-2-1013-1	106.4	38.4	38.8	39.8	100.4	21.1	89.3	59.2	66.5	1.3	44.5
25	CR-3631-1-3	91.4	26.7	37.9	40.8	106.1	24.8	135.9	113.0	82.7	2.2	229.5
26	CB 09 512	92.4	27.1	38.0	41.7	96.3	23.5	68.1	37.6	56.3	1.7	198.2
27	CR 3632-1-2	91.4	30.5	38.8	40.6	104.3	24.5	162.5	144.2	88.3	2.3	328.2
28	CR 3634-1-3	89.4	31.1	38.3	42.0	92.9	23.2	160.3	127.8	79.7	2.3	319.5
29	Anjali	69.4	30.8	38.6	41.6	88.6	23.4	127.3	116.8	90.8	2.5	274.5
30	Neha	71.4	26.2	38.0	38.4	52.8	19.7	49.5	37.6	74.2	2.2	77.0
31	CR Dhan 40	75.4	33.4	38.6	33.7	113.1	24.2	139.3	106.8	76.6	1.9	228.2
32	Poomima	79.4	22.1	36.9	40.1	74.1	20.0	107.3	93.8	86.3	2.1	205.7
33	R 2212-RF-75	82.3	30.6	38.5	38.6	87.2	19.7	129.8	100.6	78.0	2.1	235.7
34	R 1033-968-2-1	85.3	29.0	39.8	39.6	93.6	22.4	79.8	57.2	72.8	2.2	175.7
35	R 1744-4901-1-1-510-1	94.3	23.3	40.5	37.7	85.6	21.4	66.4	43.0	66.7	2.0	107.0
36	R-RHZ-2	85.3	29.4	43.0	40.4	99.6	20.2	134.8	116.6	86.6	2.4	310.7

37	R-RF 105	90.3	28.5	38.0	39.6	108.5	21.7	142.8	123.6	86.6	2.1	320.7
38	R 1670-3269-2-3926-1	94.3	28.2	37.7	44.9	94.1	20.8	131.8	104.6	79.8	2.1	264.5
39	R 1678-1901-1-1473-1	95.3	25.0	37.9	45.0	89.3	21.8	111.8	92.6	83.1	2.2	208.2
40	R 1902-912-2-512-1	93.3	28.5	37.0	44.0	88.4	21.0	125.8	109.6	87.2	1.9	277.0
41	R 1695-270-2-133-1	88.3	32.6	37.3	46.4	84.4	20.5	78.4	56.2	72.9	2.3	249.5
42	MTU 1010	94.3	27.8	36.6	40.4	86.3	20.0	77.8	62.8	81.2	2.2	167.0
43	R 1598-483-1-297-1	97.3	24.4	36.6	41.1	79.8	21.8	89.0	63.8	72.7	2.2	117.0
44	R 1570-2649-1-1546-1	94.3	24.3	34.6	39.6	79.7	21.7	136.2	91.4	68.0	2.0	194.5
45	R 1670-3975-1-485-1	94.3	25.1	34.6	40.8	78.4	21.5	84.2	50.6	62.0	2.1	165.7
46	R 1570-2644-2-1547-1	95.3	24.5	39.3	38.6	94.1	23.0	141.8	99.6	71.0	1.8	149.5
47	IGKVR 1	101.3	24.6	38.0	39.8	85.2	21.9	77.4	58.8	76.9	2.5	100.7
48	R 1702-3677-1-4734-1	93.3	25.5	38.4	42.2	86.0	22.3	116.8	85.2	73.7	2.0	119.5
49	R 741-1-55-2-1-R-1	108.3	24.4	39.9	39.1	101.0	21.8	72.8	54.2	75.5	1.9	25.7
50	Chandrasini	94.3	26.0	36.3	43.2	81.1	23.5	105.4	71.8	69.2	1.9	109.5
51	R-RHZ-LI-22	111.3	25.4	39.5	38.9	101.5	22.0	66.4	41.6	64.8	2.2	82.0
52	R 1432-251-103-1-1	93.3	28.3	37.6	38.5	90.2	23.7	131.4	108.0	82.5	1.7	173.2
53	IGKVR 1244	105.3	24.9	34.8	39.6	88.4	23.9	112.2	75.2	68.1	2.3	52.0
54	Mahamaya	94.3	26.4	27.9	40.1	90.6	21.9	73.2	41.2	58.7	1.9	73.2
55	R 1700-2243-2-2312-1	89.1	26.5	38.9	41.4	84.8	22.9	110.2	84.3	76.3	2.1	139.3
56	R 1641-914-1-400-1	107.1	23.6	41.4	35.8	87.1	22.5	88.2	59.9	66.5	1.8	93.0
57	IGKVR 2	90.1	25.2	40.6	36.8	95.0	19.7	99.8	83.5	84.1	2.3	106.8
58	R 1747-4941-1-515-1	88.1	32.4	38.4	36.7	92.6	21.9	128.0	86.9	67.1	2.7	108.0
59	CGR-547 (Bargi)	80.1	36.2	41.0	34.8	136.5	24.0	174.2	146.7	84.7	2.5	361.8
60	Anjan I	95.1	28.3	34.3	35.6	126.5	23.6	82.0	53.5	63.4	1.6	83.0
61	Badshah Bhog II	92.1	35.0	34.8	37.9	135.5	22.5	130.6	65.3	47.9	2.0	88.0
62	Jogi Bhog	93.1	30.1	36.6	35.0	144.0	22.7	92.4	59.7	62.9	2.2	123.0
63	Anjan II	93.1	44.7	37.6	36.9	153.8	24.7	144.2	104.7	72.3	2.4	230.5
64	Anjan	94.1	30.1	40.4	39.2	128.6	26.5	119.2	64.1	51.7	1.9	120.5
65	Lal Banko	89.7	31.8	38.4	36.8	139.9	25.1	137.6	69.6	48.8	2.4	100.0
66	Mudi Banko	95.7	31.0	35.1	39.9	130.5	25.3	173.6	81.6	45.3	2.3	72.5
67	Raj Banko	94.7	38.8	34.7	35.9	124.9	20.1	163.2	95.8	57.5	2.5	103.8
68	Byarangi	96.7	28.4	35.5	34.3	122.1	21.7	116.4	101.8	88.2	2.4	82.5
69	Barangi	97.7	30.8	33.7	34.7	128.5	23.9	171.6	86.6	48.9	2.2	101.3
70	Maubakuchi	99.7	32.8	36.9	31.6	116.3	24.9	100.4	59.8	58.1	2.0	135.0
71	Rajjiti (A)	103.7	28.6	37.5	40.6	127.3	25.3	82.2	38.0	43.1	2.1	47.5
72	Digamber Dhan	88.7	33.0	38.0	42.4	105.5	22.3	162.0	128.6	79.3	2.1	385.0
73	Dadhmairi Dhan	91.7	33.1	40.8	42.2	103.1	20.5	147.2	118.6	80.6	2.3	391.3
74	Chhota Dhan	99.7	30.4	36.0	36.6	109.1	23.4	108.0	48.2	42.0	2.0	118.8
75	Safed Lalak	86.7	28.9	35.5	38.7	94.7	21.9	85.6	63.2	73.7	2.5	157.5
76	Sitasal Dhan	87.7	29.2	42.6	39.6	91.7	23.7	100.6	59.6	57.8	2.4	260.0
77	Tewan Dhan	97.7	31.4	40.2	39.6	82.5	19.1	101.0	63.0	61.2	1.3	110.0

Appendix (H): Performance of mean grain yield and its traits of selected 32 RILs between Swarna x Basmati-370 under different N regimes for aerobic condition during wet season 2015.

Sr. No.	Entry Name	DF		CCFW		PHMT		PL		SPP						
		N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺			
1	RIL-1	84	85	89	25.1	36.1	39.4	114.5	121.0	133.0	23.2	24.5	26.1	128	132	156
2	RIL-3	88	86	87	33.5	35.1	38.1	96.4	104.4	112.9	26.5	23.5	27.6	131	123	127
3	RIL-21	89	90	91	32.3	34.3	37.8	88.7	105.1	123.8	22.2	23.8	24.6	150	128	165
4	RIL-33	88	85	87	29.2	31.5	40.9	107.1	125.3	136.6	23.8	26.8	29.0	148	151	162
5	RIL-34	94	97	99	34.1	37.6	39.2	91.4	112.4	111.5	20.8	24.7	24.3	146	171	163
6	RIL-35	93	95	93	35.2	38.9	41.2	83.7	111.6	112.3	19.1	23.5	25.8	134	148	153
7	RIL-36	90	86	85	36.1	38.7	39.7	92.2	109.8	124.0	22.4	25.3	26.6	149	135	128
8	RIL-37	86	89	89	28.6	37.6	40.8	108.4	113.9	115.3	23.1	26.3	25.1	108	142	128
9	RIL-44	91	92	94	35.5	38.6	41.1	106.4	113.2	115.6	22.4	23.3	26.2	172	147	137
10	RIL-59	82	80	80	30.6	36.9	37.8	84.6	98.7	102.0	21.4	23.3	23.4	147	125	133
11	RIL-70	82	84	85	23.3	34.6	35.3	102.6	101.1	122.4	22.2	23.2	24.2	151	140	116
12	RIL-74	82	82	80	31.2	37.8	38.5	110.2	138.2	123.0	25.6	23.8	25.5	134	114	175
13	RIL-78	82	87	87	36.1	38.5	37.0	115.6	125.6	121.6	26.5	25.8	25.6	155	143	169
14	RIL-91	81	82	80	37.8	38.5	40.6	121.0	132.5	132.6	27.6	25.3	27.6	115	113	150
15	RIL-93	86	88	90	35.5	36.5	38.1	81.3	95.3	94.8	21.6	19.5	22.8	149	150	160
16	RIL-97	86	81	83	37.2	43.6	43.8	123.0	130.2	132.5	26.0	24.5	25.4	169	146	143
17	RIL-107	84	86	84	33.3	34.6	37.5	85.4	96.0	85.0	20.6	23.1	22.2	124	147	153
18	RIL-112	90	88	89	35.6	40.0	38.0	126.8	133.4	138.2	28.2	30.6	27.8	156	147	133
19	RIL-115	82	82	82	31.2	31.6	31.9	125.1	135.2	137.8	23.0	21.2	24.4	130	133	125
20	RIL-134	86	88	88	35.1	43.3	40.2	133.6	144.5	142.0	24.6	26.8	25.0	169	166	145
21	RIL-138	80	81	80	37.2	42.4	45.1	117.3	127.4	128.3	25.2	23.8	26.4	144	142	145
22	RIL-147	82	82	84	35.8	38.4	42.7	85.6	78.1	84.6	22.8	22.9	21.8	140	144	125
23	RIL-149	86	87	92	36.2	36.5	38.1	107.0	140.8	139.2	25.3	25.4	24.2	107	135	150
24	RIL-159	86	83	95	32.2	34.9	35.6	118.6	121.0	127.0	23.4	24.0	21.7	107	111	114
25	RIL-164	89	89	91	36.1	41.5	41.6	117.3	122.2	137.4	26.8	26.9	28.5	143	147	133
26	RIL-169	86	86	87	33.2	35.3	34.6	123.8	123.8	135.4	27.3	27.6	24.2	144	142	155
27	RIL-170	94	97	100	29.5	36.3	34.9	97.8	111.3	105.2	22.0	23.9	21.3	145	145	115
28	RIL-172	81	82	82	30.2	39.5	40.4	108.4	126.9	130.2	28.5	29.2	27.8	152	150	163
29	RIL-174	78	77	78	29.8	40.6	43.8	76.8	88.4	102.0	21.5	21.5	25.6	113	139	147
30	RIL-175	87	90	93	32.9	35.4	39.9	121.6	138.2	141.2	23.9	27.9	27.0	132	139	147
31	RIL-177	86	82	88	32.4	41.5	45.2	126.8	128.0	130.2	28.9	28.0	29.8	135	140	154
32	RIL-178	84	84	89	27.1	36.3	40.8	109.6	124.9	132.2	28.1	32.4	28.1	139	160	149

S.N.	Entry Name	SPP						FGP						SF (%)					
		Aerobic			Anaerobic			Aerobic			Anaerobic			Aerobic			Anaerobic		
		N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺
1	Indira Sona	122.00	104.83	114.17	193.90	178.50	162.70	102.00	74.83	95.33	158.10	151.80	133.80	83.66	71.14	83.52	81.57	84.94	82.36
2	Indira Aerobic 1	99.33	95.50	131.17	199.30	182.60	166.50	80.50	78.67	102.67	175.70	158.50	150.60	81.07	82.05	78.31	88.15	86.80	90.41
3	Swarna	103.83	116.67	96.33	193.80	143.40	204.40	85.00	98.83	69.50	171.50	121.70	181.70	81.83	84.90	72.14	88.50	84.86	88.89
4	Basmati- 370	110.83	98.33	110.00	114.10	99.90	117.60	93.17	83.50	77.17	96.60	80.90	107.20	84.10	85.01	71.12	84.71	81.04	91.28
5	IR-64 Drought	93.00	99.00	98.17	116.90	117.30	116.00	75.83	84.33	76.67	108.80	96.80	104.70	81.72	84.96	78.28	93.13	82.32	90.48
6	Samleshwari	102.33	104.67	106.67	125.10	132.80	131.10	82.83	82.83	80.00	112.60	119.00	119.20	80.98	79.13	75.03	89.94	89.64	90.96
7	Danteshwari	110.50	83.83	95.83	104.70	105.50	125.80	84.00	70.50	79.00	95.80	88.60	104.00	75.65	84.14	82.38	91.49	83.32	82.65
8	RP 5125-2-4	110.67	119.17	99.50	175.60	169.30	181.30	92.67	98.17	80.17	155.50	151.30	160.60	83.81	82.83	80.50	88.51	89.44	88.60
9	R 1779-321-1-112-1	107.67	119.00	98.17	119.50	130.10	168.10	87.50	96.00	73.33	106.20	111.80	150.10	81.12	81.07	74.69	88.94	85.81	89.27
10	R 1882-306-4-243-1	126.33	101.83	102.67	177.20	197.10	171.90	108.33	70.83	74.83	163.50	174.60	154.20	85.81	69.38	72.89	92.25	88.58	89.68
11	R 2093-1536-1-660-1	99.67	101.83	111.50	128.70	148.30	143.80	78.67	79.67	90.33	114.50	123.40	119.00	78.87	78.32	81.43	88.79	83.88	82.73
12	IR 84887-B-15	93.00	129.33	119.17	154.70	173.50	155.70	74.17	95.33	89.17	137.00	160.40	135.90	79.80	73.52	74.73	88.62	92.30	87.25
13	IR 83376-B-B-110-3	93.33	89.33	83.00	168.20	120.30	144.60	79.17	70.33	62.50	140.30	106.30	131.90	84.76	78.78	75.34	83.37	88.03	91.20
14	R 1700-309-1-171-1	83.50	117.83	91.67	173.20	166.00	164.60	63.33	87.50	60.00	144.00	154.60	140.20	75.77	74.04	65.58	83.06	93.16	85.19
15	R 1672-1171-1-124-1	112.83	101.33	94.33	144.30	171.20	136.40	96.00	81.00	76.17	123.90	160.20	123.80	85.06	79.84	80.98	85.83	93.75	90.77
16	R 1262-1667-1-1	97.00	92.17	88.50	151.70	122.70	157.70	78.17	76.50	75.17	129.70	109.10	135.80	80.43	82.97	84.74	85.40	88.97	86.09
17	R 1860-783-1-424-1	102.67	105.83	119.50	169.80	153.70	199.90	82.83	84.83	93.50	164.00	145.00	179.10	80.80	80.10	78.30	96.76	94.37	89.53
18	RAU 1484-Aer-04	116.67	123.33	106.83	183.20	149.30	161.20	98.17	96.83	90.83	141.80	130.40	138.70	84.13	78.44	84.97	77.32	87.36	86.04
19	RCPR 8	110.00	92.33	113.83	186.10	120.00	141.00	90.33	75.67	81.50	165.10	96.70	134.90	82.09	81.97	71.56	88.72	80.49	95.60
20	CR 3631-1-3	109.17	103.00	111.17	128.90	133.00	127.70	90.50	86.67	83.67	113.30	120.70	110.30	82.99	84.22	75.10	87.91	90.74	86.36
21	CR 3632-1-2	103.67	103.00	101.17	120.20	117.10	146.50	89.83	84.00	84.33	94.10	102.20	125.80	86.67	81.57	83.47	78.09	87.47	85.87
22	CR 3634-1-3	106.67	105.50	110.67	135.50	148.90	155.00	90.00	82.50	92.00	111.80	121.70	131.00	84.44	78.85	83.23	82.52	81.85	84.49
23	CR Dhan 40	101.33	127.17	102.00	186.70	131.60	184.00	75.17	101.50	85.00	168.20	115.40	173.10	73.89	80.04	83.37	90.09	87.77	94.08
24	R-RHZ-2	97.67	103.17	119.83	150.20	122.90	117.40	77.00	78.67	97.67	135.90	99.70	99.30	78.79	76.12	81.84	90.49	80.94	84.58
25	R-RF 105	103.67	101.00	102.17	174.40	164.70	174.40	81.00	85.83	85.17	157.60	158.20	156.90	78.00	84.95	83.09	90.39	96.12	89.94
26	R 1670-3269-2-3926-1	93.00	98.17	107.33	141.10	146.60	136.00	78.33	84.00	90.83	125.40	130.70	127.30	84.26	85.69	84.58	88.87	89.12	93.63
27	R 1902-912-2-512-1	107.50	113.83	99.50	145.10	134.90	118.30	91.00	92.17	82.17	122.20	115.40	99.70	84.66	81.19	82.57	84.22	85.58	84.23
28	MTU-1010	104.17	101.50	93.33	111.00	104.70	174.30	82.33	85.50	77.83	94.50	92.50	158.30	79.35	84.25	83.11	85.06	88.35	90.87
29	R 1570-2644-2-1547-1	116.33	97.67	136.17	191.40	162.10	196.50	94.83	81.83	103.00	169.60	139.20	179.60	81.45	83.82	75.65	88.61	85.88	91.47
30	R 1432-251-103-1-1	119.00	102.33	127.17	100.40	127.60	128.50	94.83	85.00	91.67	90.20	111.50	118.60	79.72	83.08	72.05	89.67	87.35	92.24
31	CGR-547 (Bargi)	104.00	105.50	99.83	103.70	125.60	116.30	87.67	88.50	82.33	91.00	115.80	101.50	84.21	83.94	82.53	87.67	92.45	87.29
32	Digamber Dhan	86.83	95.50	97.17	140.90	148.10	119.20	65.33	74.33	78.33	130.80	138.00	111.30	75.35	77.68	80.56	92.80	93.22	93.55
33	Dadmaini Dhan	99.17	95.83	121.33	138.60	144.60	130.30	79.67	81.83	102.33	124.80	136.40	123.80	80.12	85.37	84.36	89.92	94.35	95.09
34	CR Dhan 201	103.17	98.00	109.83	107.40	126.00	129.50	77.67	78.17	85.83	96.60	118.90	119.00	75.26	79.69	78.44	90.38	94.35	92.06
35	CR Dhan 202	111.17	101.17	102.50	139.00	157.30	193.70	94.17	81.00	85.50	127.00	140.50	182.20	84.72	79.84	83.31	91.36	89.24	93.98
36	IR-64	106.67	93.33	96.50	108.40	114.10	142.20	85.33	72.67	73.00	95.30	104.50	130.70	80.12	78.02	75.62	87.86	91.50	91.85
37	Indira Barani Dhan 1	102.50	103.83	105.17	149.80	179.00	124.50	86.50	86.17	80.17	136.00	156.40	111.10	84.42	82.97	75.97	90.82	87.34	89.19
38	Sampada	95.83	120.67	125.83	117.70	189.20	183.40	76.83	99.50	103.33	95.00	167.50	162.20	80.10	82.72	82.12	80.61	88.51	88.42
	SED	7.82	8.19	10.33	10.21	10.98	10.36	7.63	7.15	8.66	9.73	9.37	9.71	4.59	4.61	4.93	2.09	3.33	2.14
	CD	15.84	16.60	20.94	20.68	22.24	20.99	15.45	14.48	17.54	19.72	18.99	19.66	9.31	9.35	8.48	4.23	6.76	4.33
	CV	7.49	7.85	9.70	6.96	7.64	6.85	8.97	8.50	10.31	7.57	7.38	7.19	5.65	5.72	5.62	2.38	3.78	2.40

S.N.	Traits		HI (%)						CCFW						GNC (%)						Appendix (I) continued...	
			Aerobic			Anaerobic			Aerobic			Anaerobic			Aerobic			Anaerobic				
	Entry Name		N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺		
1	Indira Sona		20.30	22.40	17.96	27.38	27.75	27.69	29.18	36.25	36.35	31.30	32.70	33.90	1.20	1.37	1.58	0.89	1.16	1.19		
2	Indira Aerobic 1		29.79	30.12	25.99	31.83	29.09	28.71	29.98	38.43	35.75	32.45	32.85	34.40	1.26	1.42	1.66	1.02	1.01	1.24		
3	Swarna		6.58	7.22	7.74	25.74	27.87	27.14	32.95	37.60	38.15	34.17	38.50	39.50	1.28	1.37	1.72	1.06	1.20	1.39		
4	Basmati- 370		21.33	14.82	17.29	28.48	17.90	21.89	34.08	38.08	37.70	32.42	34.50	35.60	1.32	1.50	1.46	1.03	1.00	1.28		
5	IR-64 drought		38.80	37.48	28.86	27.67	29.52	23.32	32.71	38.29	37.35	30.83	35.60	38.05	1.20	1.48	1.55	0.91	1.11	1.11		
6	Samleshwari		31.64	33.91	30.07	29.58	36.07	31.33	25.63	37.39	38.70	32.00	33.95	38.90	1.29	1.43	1.63	0.97	1.13	1.62		
7	Danteshwari		34.50	31.60	31.07	34.86	43.39	36.57	29.58	34.05	34.35	31.17	32.40	42.40	1.02	1.46	1.72	0.71	0.89	1.23		
8	RP 5125-2-4		36.75	34.88	33.64	33.77	34.60	26.93	35.73	41.94	41.80	35.75	39.10	38.40	1.27	1.51	1.77	0.99	1.14	1.18		
9	R 1779-321-1-112-1		23.29	24.93	21.43	32.85	32.53	22.68	33.26	42.13	44.50	31.60	35.55	37.70	1.01	1.06	1.21	0.79	0.92	1.25		
10	R 1882-306-4-243-1		30.82	36.34	32.35	33.22	34.82	30.25	35.30	41.43	40.80	33.95	38.25	39.65	1.37	1.62	1.76	1.06	1.23	1.30		
11	R 2093-1536-1-660-1		34.53	28.20	30.06	34.57	28.07	28.44	32.89	41.23	38.85	36.03	38.15	37.90	1.30	1.33	1.53	0.99	1.13	1.27		
12	IR 84887-B-15		32.48	30.80	34.72	31.24	29.76	33.24	31.85	36.16	38.15	38.18	39.20	39.00	1.34	1.48	1.58	0.73	0.91	1.21		
13	IR 83376-B-B-110-3		41.75	26.30	23.97	36.12	26.90	34.17	34.26	39.20	37.95	35.08	37.15	43.70	1.20	1.35	1.61	1.00	1.18	1.20		
14	R 1700-309-1-171-1		34.53	23.47	21.94	29.21	32.59	32.73	27.51	39.75	42.80	31.97	34.60	41.40	1.15	1.39	1.54	0.95	1.13	1.13		
15	R 1672-1171-1-124-1		30.71	27.88	23.66	30.94	26.37	27.38	31.31	46.01	41.15	33.20	33.05	33.95	1.20	1.39	1.59	0.98	1.13	1.17		
16	R 1262-1667-1-1		34.50	25.94	28.75	26.15	28.97	23.08	27.48	41.73	40.40	33.40	34.60	40.70	1.13	1.29	1.67	0.64	0.73	1.10		
17	R 1860-783-1-424-1		29.73	29.95	28.02	33.79	34.71	26.07	32.29	40.30	40.85	34.57	36.15	36.00	1.13	1.32	1.46	0.88	1.03	1.03		
18	RAU 1484-Aer-04		53.70	25.73	25.89	25.88	28.36	25.55	34.23	40.59	40.85	37.72	40.40	44.20	1.23	1.44	1.72	0.99	1.06	1.46		
19	RCPR 8		44.35	40.65	31.41	31.49	32.37	29.11	31.06	40.18	38.65	35.00	35.20	39.70	1.42	1.39	1.58	0.85	1.00	1.39		
20	CR 3631-1-3		49.58	52.48	34.44	34.28	38.37	32.09	24.86	37.95	37.00	34.40	37.05	41.40	1.38	1.61	1.69	0.85	1.06	1.45		
21	CR 3632-1-2		53.74	34.83	27.44	35.33	34.65	31.33	35.20	35.39	33.30	35.38	36.50	42.10	1.09	1.62	1.71	0.95	1.16	1.43		
22	CR 3634-1-3		32.39	30.42	30.68	22.25	26.74	26.39	35.30	37.13	38.55	36.83	38.50	38.50	1.32	1.66	1.64	0.86	0.99	1.13		
23	CR Dhan 40		63.64	44.03	46.22	28.76	37.87	29.36	36.23	42.05	44.05	32.60	34.05	35.05	0.90	0.98	1.02	0.64	0.82	0.88		
24	R-RHZ-2		31.67	39.06	34.64	22.98	30.19	31.70	31.61	35.46	35.30	34.15	35.75	35.95	1.20	1.40	1.61	0.99	1.05	1.19		
25	R-RF 105		34.83	25.48	30.62	31.46	31.31	31.47	37.28	40.74	36.90	35.97	36.10	38.25	1.09	1.26	1.72	0.85	1.11	1.18		
26	R 1670-3269-2-3926-1		33.58	24.69	29.68	38.18	31.04	33.15	36.11	39.19	37.75	36.00	37.50	37.25	1.06	1.23	1.32	0.88	0.99	1.12		
27	R 1902-912-2-512-1		27.14	28.92	26.70	41.94	29.49	31.52	38.00	40.31	40.20	34.45	39.05	39.60	1.23	1.33	1.70	1.02	1.24	1.20		
28	MTU-1010		33.17	17.05	17.07	34.10	33.16	29.50	35.49	43.51	42.75	31.98	35.95	37.70	0.97	1.19	1.13	0.58	0.75	0.99		
29	R 1570-2644-2-1547-1		35.90	25.53	26.31	34.20	30.45	28.73	40.18	41.26	35.70	32.77	32.90	34.25	1.20	1.18	1.59	0.97	0.97	1.09		
30	R 1432-251-103-1-1		36.82	17.29	16.06	32.37	31.12	25.00	31.51	37.29	42.45	31.53	33.30	37.85	1.20	1.16	1.62	1.02	1.04	1.18		
31	CGR-547 (Bargi)		49.71	35.02	32.79	27.14	28.90	23.81	31.40	39.34	38.45	32.93	32.95	35.60	1.15	1.12	1.53	0.63	0.82	1.16		
32	Digamber Dhan		41.74	41.72	31.92	25.71	34.21	25.65	37.80	36.80	42.90	33.85	36.30	38.35	1.27	1.31	1.51	0.94	1.07	1.08		
33	Dadmaini Dhan		46.41	30.89	30.81	30.40	32.03	34.75	35.18	39.01	39.70	32.72	35.85	37.55	1.20	1.31	1.55	0.97	1.03	1.07		
34	CR Dhan 201		28.17	30.51	19.09	38.06	35.47	32.67	28.95	35.10	31.50	31.77	33.20	37.45	1.32	1.34	1.66	0.88	1.09	1.06		
35	CR Dhan 202		41.31	24.49	13.39	32.93	38.63	35.25	26.61	34.00	34.25	30.72	33.95	41.95	1.30	1.39	1.72	0.99	1.07	1.18		
36	IR-64		37.68	35.43	22.66	32.64	29.19	30.00	24.98	34.15	31.20	35.15	36.90	41.90	1.31	1.42	1.70	0.90	1.00	1.06		
37	Indira Barani Dhan 1		35.17	31.88	16.87	36.07	39.99	31.78	25.36	35.50	37.55	29.95	32.45	35.85	1.33	1.42	1.70	0.82	0.92	1.18		
38	Sampada		14.02	17.47	11.82	25.79	23.88	30.36	30.79	34.73	33.80	30.33	35.20	35.15	1.29	1.47	1.41	0.83	0.90	1.25		
SED			5.42	4.52	3.44	2.56	2.10	1.71	2.44	1.53	2.37	2.16	2.48	1.96	0.04	0.05	0.06	0.04	0.04	0.05		
CD			10.99	9.16	6.96	5.18	4.26	3.47	4.93	3.10	4.79	4.37	5.03	3.97	0.08	0.10	0.11	0.08	0.08	0.09		
CV			15.41	15.35	13.14	8.17	6.66	5.86	7.56	3.96	6.18	6.44	6.96	5.11	3.37	3.57	3.52	4.44	3.80	3.81		

S.N.	Traits	GPC (%)						SNC (%)						GNY (g/m ²)					
		Aerobic			Anaerobic			Aerobic			Anaerobic			Aerobic			Anaerobic		
		N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺
1	Indira Sona	7.16	8.12	9.37	5.29	6.87	7.08	0.81	0.92	1.05	0.57	0.68	0.72	2.21	3.18	3.72	4.81	6.54	8.53
2	Indira Aerobic 1	7.50	8.45	9.87	6.08	6.00	7.37	0.84	0.92	1.07	0.59	0.73	0.76	2.43	3.78	4.35	5.60	5.24	6.56
3	Swarna	7.62	8.16	10.20	6.33	7.12	8.25	0.99	1.17	1.27	0.71	0.74	0.88	0.55	0.80	1.46	4.65	6.70	7.17
4	Basmati- 370	7.87	8.91	8.70	6.12	5.96	7.62	0.85	1.07	1.10	0.62	0.77	0.85	1.74	2.01	2.86	3.90	2.72	5.32
5	IR-64 Drought	7.12	8.79	9.25	5.41	6.58	6.62	0.75	0.88	1.08	0.48	0.64	0.74	2.72	3.97	4.67	3.22	4.97	4.44
6	Samleshwari	7.66	8.50	9.70	5.79	6.71	9.66	0.88	1.02	1.38	0.61	0.71	0.77	2.53	3.70	4.86	3.42	5.47	8.43
7	Danteshwari	6.04	8.70	10.20	4.25	5.29	7.33	0.60	0.75	0.85	0.60	0.63	0.75	1.44	2.98	3.83	1.77	3.20	3.88
8	RP 5125-2-4	7.58	9.00	10.54	5.91	6.79	7.04	0.92	0.99	1.21	0.51	0.72	0.78	3.11	4.22	5.50	5.28	6.39	6.81
9	R 1779-321-1-112-1	6.00	6.33	7.21	4.71	5.50	7.46	0.82	0.93	1.13	0.46	0.70	0.76	1.58	1.93	2.33	4.48	4.85	5.69
10	R 1882-306-4-243-1	8.12	9.62	10.50	6.29	7.29	7.71	0.99	1.11	1.13	0.64	0.69	0.74	2.61	4.39	4.55	6.52	6.57	7.21
11	R 2093-1536-1-660-1	7.71	7.91	9.12	5.91	6.71	7.58	0.91	0.96	1.05	0.61	0.78	0.81	2.15	2.11	2.88	5.21	4.49	5.96
12	IR 84887-B-15	7.96	8.79	9.41	4.33	5.41	7.21	0.70	0.99	1.02	0.68	0.83	0.80	1.88	2.90	3.68	4.50	5.27	7.80
13	IR 83376-B-B-110-3	7.16	8.04	9.58	5.96	7.04	7.16	0.71	0.76	0.80	0.57	0.64	0.72	1.59	2.21	3.26	5.96	5.46	7.48
14	R 1700-309-1-171-1	6.83	8.29	9.16	5.62	6.75	6.71	0.72	0.81	0.95	0.54	0.59	0.76	1.85	2.39	3.26	4.43	7.35	7.26
15	R 1672-1171-1-124-1	7.16	8.25	9.45	5.83	6.71	6.96	0.62	0.88	0.90	0.58	0.69	0.74	1.92	2.44	3.85	5.06	5.10	5.59
16	R 1262-1667-1-1	6.71	7.66	9.91	3.83	4.33	6.54	0.82	0.85	0.98	0.43	0.53	0.63	1.30	1.98	3.32	2.45	3.59	4.51
17	R 1672-1667-1-1	6.71	7.83	8.66	5.25	6.12	6.12	0.85	0.92	0.97	0.59	0.69	0.76	1.41	1.97	2.73	4.91	5.73	4.18
18	RAU 1484-Aer-04	7.29	8.54	10.20	5.87	6.33	8.66	0.94	0.95	1.27	0.62	0.64	0.76	2.46	3.47	4.51	4.44	5.60	7.56
19	RCPR 8	8.45	8.25	9.41	5.08	5.96	8.25	0.91	0.99	0.97	0.50	0.55	0.69	2.68	3.57	4.61	5.19	6.49	9.26
20	CR 3631-1-3	8.21	9.58	10.08	5.04	6.29	8.62	0.92	0.99	1.14	0.60	0.75	0.77	2.57	4.12	5.18	3.80	5.12	8.39
21	CR 3632-1-2	6.50	9.62	10.16	5.66	6.87	8.50	0.88	0.99	1.04	0.57	0.71	0.76	2.05	3.72	4.48	4.36	4.58	8.35
22	CR 3634-1-3	7.87	9.87	9.75	5.12	5.91	6.71	0.76	0.91	0.88	0.49	0.55	0.68	2.05	2.98	3.25	2.92	4.06	5.49
23	CR Dhan 40	5.37	5.83	6.04	3.79	4.87	5.25	0.54	0.61	0.74	0.48	0.50	0.64	1.07	1.33	1.61	2.22	3.14	3.43
24	R-RHZ-2	7.12	8.33	9.58	5.87	6.25	7.08	0.88	1.02	0.99	0.61	0.78	0.83	1.29	2.41	2.81	2.83	4.26	4.98
25	R-RF 105	6.50	7.50	10.20	5.08	6.58	7.04	0.77	0.90	0.99	0.47	0.74	0.75	1.05	1.79	3.60	3.75	5.24	6.32
26	R 1670-3269-2-3926-1	6.33	7.29	7.83	5.21	5.91	6.66	0.82	0.93	0.99	0.52	0.74	0.83	1.44	2.25	3.31	4.59	4.17	6.30
27	R 1902-912-2-512-1	7.33	7.91	10.12	6.04	7.37	7.16	0.94	0.95	1.01	0.63	0.73	0.76	1.26	1.95	3.26	4.70	4.03	5.86
28	MTU-1010	5.79	7.08	6.71	3.46	4.46	5.87	0.60	0.85	0.88	0.42	0.64	0.71	1.13	1.68	1.83	2.65	3.28	4.54
29	R 1570-2644-2-1547-1	7.16	7.04	9.45	5.79	5.79	6.50	0.82	0.86	0.96	0.56	0.65	0.71	1.56	2.19	3.98	5.61	4.13	6.04
30	R 1432-251-103-1-1	7.16	6.87	9.62	6.08	6.21	7.00	0.78	0.92	0.99	0.57	0.74	0.81	1.70	1.77	2.39	4.93	3.62	4.06
31	CGR-547 (Bargi)	6.83	6.66	9.08	3.75	4.87	6.87	0.83	0.88	0.99	0.43	0.75	0.84	1.72	1.86	3.08	2.67	3.17	4.71
32	Digamber Dhan	7.54	7.79	8.95	5.58	6.37	6.41	0.79	0.97	0.96	0.58	0.77	0.80	2.20	2.56	2.99	2.40	4.82	3.99
33	Dadmaini Dhan	7.12	7.79	9.20	5.79	6.12	6.37	0.85	0.99	1.02	0.53	0.80	0.82	1.92	2.44	3.39	3.23	4.26	5.12
34	CR Dhan 201	7.87	8.00	9.87	5.25	6.46	6.29	0.90	0.99	1.03	0.62	0.74	0.83	1.73	2.52	3.13	3.08	4.93	4.18
35	CR Dhan 202	7.75	8.25	10.20	5.91	6.37	7.00	0.80	0.94	1.07	0.61	0.71	0.77	1.85	2.59	2.55	4.00	6.36	6.29
36	IR-64	7.79	8.45	9.75	5.37	5.96	6.33	0.99	1.09	1.02	0.62	0.75	0.83	1.87	2.44	3.33	2.99	4.55	4.15
37	Indira Barani Dhan 1	7.91	8.45	10.12	4.87	5.50	7.04	0.76	1.06	1.09	0.62	0.68	0.77	1.70	2.39	2.57	3.33	5.09	5.27
38	Sampada	7.66	8.75	8.37	4.91	5.37	7.46	0.92	1.01	1.11	0.49	0.73	0.77	0.58	1.28	1.32	2.54	3.15	5.16
SED		0.24	0.29	0.33	0.24	0.23	0.27	0.03	0.04	0.03	0.05	0.04	0.04	0.19	0.26	0.30	0.25	0.31	0.41
CD		0.49	0.59	0.67	0.48	0.47	0.55	0.07	0.08	0.06	0.10	0.08	0.09	0.38	0.53	0.60	0.50	0.63	0.83
CV		3.37	3.57	3.52	4.44	3.80	3.81	4.22	3.98	3.14	8.39	5.81	5.63	10.45	10.11	8.74	6.16	6.44	6.89

Appendix (I) continued...

S.N.	Entry Name	SNY (g/m ²)						BNY (g/m ²)						NHI (%)					
		Aerobic			Anaerobic			Aerobic			Anaerobic			Aerobic			Anaerobic		
		N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺
1	Indira Sona	5.87	7.50	11.34	8.14	10.01	13.45	8.08	10.69	15.07	12.96	16.55	21.98	27.41	29.88	24.74	37.17	39.50	38.74
2	Indira Aerobic 1	3.81	5.80	7.98	6.90	9.28	9.93	6.24	9.58	12.33	12.50	14.52	16.49	38.89	40.14	35.22	44.79	36.21	39.76
3	Swarna	6.02	8.79	12.79	8.92	10.64	12.17	6.57	9.58	14.25	13.57	17.35	19.35	8.38	8.38	10.21	34.27	38.65	37.07
4	Basmati- 370	4.17	8.35	10.28	5.95	9.61	12.55	5.91	10.36	13.13	9.84	12.33	17.88	29.52	21.77	39.65	22.09	29.76	
5	IR-64 Drought	2.74	4.01	6.52	4.44	6.88	9.74	5.46	7.98	11.19	7.65	11.85	14.18	50.26	50.17	41.75	42.22	41.79	31.32
6	Samleshwari	3.79	5.15	9.58	5.07	6.08	8.76	6.32	8.85	14.44	8.50	11.55	17.19	40.43	41.89	33.67	40.16	47.35	49.05
7	Danteshwari	1.62	3.33	4.21	2.76	2.97	4.07	3.06	6.32	8.04	4.53	6.17	7.94	47.25	47.41	47.71	39.10	51.95	48.71
8	RP 5125-2-4	3.89	5.21	7.44	5.39	7.63	12.25	7.00	9.43	12.95	10.67	14.02	19.06	44.47	44.82	42.55	49.83	45.58	35.74
9	R 1779-321-1-112-1	4.22	5.07	7.98	5.26	7.62	11.86	5.79	7.00	10.31	9.74	12.48	17.55	27.22	27.52	22.68	45.97	38.88	32.66
10	R 1882-306-4-243-1	4.34	5.35	6.10	7.92	6.98	9.44	6.95	9.74	10.66	14.44	13.54	16.65	37.91	45.23	42.66	45.23	48.54	43.33
11	R 2093-1536-1-660-1	2.88	4.13	4.75	6.05	8.01	9.57	5.03	6.23	7.63	11.26	12.50	15.53	42.87	35.18	38.42	46.29	35.94	38.44
12	IR 84887-B-15	2.05	4.61	4.44	9.26	11.42	10.33	3.93	7.52	8.12	13.76	16.69	18.13	47.97	39.60	45.32	32.76	31.62	43.02
13	IR 83376-B-B-110-3	1.32	3.55	5.12	6.15	7.94	8.66	2.91	5.76	8.38	12.11	13.39	16.14	54.90	38.68	38.86	49.56	40.55	46.40
14	R 1700-309-1-171-1	2.20	4.55	7.30	6.10	7.88	10.01	4.05	6.95	10.57	10.54	15.23	17.27	45.60	34.44	31.34	42.08	48.27	42.06
15	R 1672-1171-1-124-1	2.26	4.03	7.18	6.70	8.68	9.44	4.18	6.48	11.04	11.76	13.78	15.03	46.13	37.91	35.35	43.04	37.04	37.26
16	R 1262-1667-1-1	1.79	3.74	4.85	4.59	6.34	8.60	3.09	5.72	8.17	7.04	9.93	13.11	42.01	34.57	40.67	35.12	36.15	34.38
17	R 1670-783-1-424-1	2.54	3.33	4.71	6.43	7.27	8.75	3.95	5.31	7.43	11.34	13.00	12.93	35.90	37.77	36.75	43.32	44.11	32.30
18	RAU 1484-Aer-04	1.64	6.63	9.52	7.95	8.58	11.43	4.10	10.10	14.03	12.39	14.17	19.00	60.18	34.30	32.10	35.87	39.64	39.80
19	RCPR 8	2.20	3.79	6.21	6.79	7.40	11.27	4.88	7.36	10.81	11.98	13.89	20.53	55.38	48.76	42.76	43.88	46.73	45.20
20	CR 3631-1-3	2.01	2.37	6.62	5.14	5.78	9.44	4.58	6.49	11.80	8.93	10.90	17.83	58.91	64.00	43.81	42.63	46.80	47.11
21	CR 3632-1-2	1.44	4.39	7.20	4.82	5.34	9.72	3.49	8.11	11.69	9.18	9.92	18.07	58.94	46.46	38.38	47.51	46.42	46.31
22	CR 3634-1-3	2.57	3.76	3.95	5.82	6.18	9.23	4.62	6.74	7.20	8.73	10.24	14.72	45.11	44.26	45.21	33.62	39.62	37.37
23	CR Dhan 40	0.36	1.10	1.37	4.11	3.12	5.93	1.43	2.42	2.98	6.33	6.26	9.36	74.56	55.64	54.24	35.08	50.16	36.53
24	R-RHZ-2	2.07	2.73	3.31	5.86	7.28	7.51	3.36	5.14	6.11	8.69	11.53	12.48	38.70	46.88	46.20	32.59	36.93	39.90
25	R-RF 105	1.67	3.99	4.69	4.48	7.63	8.72	2.71	5.78	8.30	8.24	12.87	15.03	42.31	32.29	43.40	45.52	40.68	42.03
26	R 1670-3269-2-3926-1	2.19	5.23	6.19	4.41	6.83	9.44	3.63	7.48	9.50	9.00	11.00	15.74	39.64	30.16	35.68	51.03	37.86	40.01
27	R 1902-912-2-512-1	2.57	3.59	5.48	4.09	5.70	8.10	3.82	5.54	8.74	8.79	9.73	13.97	32.85	36.18	38.02	53.65	41.60	42.11
28	MTU-1010	1.39	5.82	6.91	3.69	5.62	7.87	2.52	7.50	8.74	6.34	8.89	12.42	44.76	22.39	20.93	41.71	36.88	36.64
29	R 1570-2644-2-1547-1	1.90	4.67	6.77	6.29	6.30	9.79	3.46	6.86	10.74	11.90	10.43	15.83	45.14	32.00	37.17	47.51	39.59	38.17
30	R 1432-251-103-1-1	1.95	6.79	7.67	5.71	5.71	8.41	3.64	8.56	10.05	10.64	9.33	12.47	47.39	20.77	23.73	46.28	38.83	32.53
31	CGR-547 (Bargi)	1.26	2.80	4.10	4.87	7.15	10.95	2.97	4.66	7.18	7.54	10.32	15.65	57.66	40.44	42.97	35.50	30.79	30.06
32	Digambar Dhan	1.92	2.64	4.09	4.29	6.68	8.56	4.11	5.20	7.08	6.70	11.49	12.54	53.43	49.22	42.37	35.84	41.92	31.77
33	Dadmaini Dhan	1.61	4.12	5.00	4.05	7.03	7.39	3.53	6.56	8.39	7.28	11.29	12.51	54.77	37.21	40.40	44.44	37.78	41.02
34	CR Dhan 201	3.17	4.18	8.28	3.50	6.07	6.72	4.90	6.69	11.40	6.58	11.00	10.90	36.51	37.38	27.58	46.90	44.79	38.29
35	CR Dhan 202	1.62	5.40	10.37	5.02	6.73	7.59	3.47	7.98	12.92	9.02	13.09	13.88	53.44	32.35	19.84	44.52	48.56	45.44
36	IR-64	2.32	3.40	7.11	4.25	8.27	7.60	4.20	5.84	10.44	7.24	12.82	11.76	44.51	41.80	31.95	41.34	35.52	35.38
37	Indira Barani Dhan 1	1.80	3.83	8.15	4.61	5.61	7.36	3.50	6.21	10.72	7.94	10.70	12.64	48.54	38.43	24.09	42.73	47.56	41.73
38	Sampada	2.56	4.24	7.78	4.33	8.23	7.33	3.14	5.52	9.10	6.87	11.38	12.49	18.52	23.68	14.49	36.90	28.11	41.49
SED		0.47	0.67	0.91	0.74	0.58	0.71	0.48	0.70	0.93	0.78	0.65	0.81	6.22	4.91	4.00	3.81	2.37	2.43
CD		0.95	1.36	1.85	1.51	1.17	1.43	0.98	1.41	1.88	1.58	1.32	1.64	12.60	9.94	8.10	7.72	4.80	4.93
CV		18.70	14.81	13.66	13.44	8.06	7.67	11.17	9.78	9.24	8.19	5.44	5.35	14.08	13.06	11.38	9.08	5.85	6.20

Appendix (I) continued...

S.N.	Entry Name	Traits		NUE (gg ⁻¹ N)						NUE (gg ⁻¹ N)					
				Aerobic			Anaerobic			Aerobic			Anaerobic		
		N ⁰	NH ₄ ⁺	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰	NO ₃ ⁻	NH ₄ ⁺	N ⁰
1	Indira Sona	0.10	0.13	0.16	0.21	0.27	22.78	21.86	41.82	34.22	32.53	2.29	2.91	2.96	6.78
2	Indira Aerobic 1	0.08	0.12	0.16	0.18	0.21	30.87	28.12	43.87	36.00	32.09	2.41	3.33	3.27	6.85
3	Swarna	0.08	0.12	0.17	0.22	0.24	6.53	6.10	32.21	32.29	26.81	0.53	0.73	1.06	5.46
4	Basmati- 370	0.07	0.13	0.12	0.15	0.22	22.36	13.06	38.50	22.07	23.23	1.64	1.68	2.44	4.73
5	IR-64 Drought	0.07	0.10	0.14	0.10	0.18	42.02	34.08	46.50	37.85	28.17	2.84	3.35	3.76	4.42
6	Samleshwari	0.08	0.11	0.18	0.14	0.21	31.35	29.41	41.27	42.01	30.20	2.46	3.24	3.73	4.39
7	Danteshwari	0.04	0.08	0.10	0.06	0.10	46.58	32.48	54.80	58.78	39.55	1.77	2.55	2.79	3.09
8	RP 5125-2-4	0.09	0.12	0.16	0.13	0.24	34.92	29.59	50.08	39.98	30.24	3.05	3.49	3.88	6.64
9	R 1779-321-1-112-1	0.07	0.09	0.13	0.12	0.22	26.87	25.85	18.71	58.14	26.00	1.95	2.26	2.41	7.07
10	R 1882-306-4-243-1	0.09	0.12	0.13	0.18	0.17	27.68	27.88	42.77	39.66	33.46	2.39	3.38	3.23	7.72
11	R 2093-1536-1-660-1	0.06	0.08	0.10	0.16	0.19	33.09	26.28	46.56	31.89	30.15	2.08	1.98	2.35	6.55
12	IR 84887-B-15	0.05	0.09	0.10	0.17	0.21	35.88	26.66	44.99	34.83	35.52	1.76	2.45	2.91	7.73
13	IR 83376-B-B-110-3	0.04	0.07	0.10	0.15	0.20	45.57	28.73	49.62	34.27	38.52	1.65	2.05	2.53	7.44
14	R 1700-309-1-171-1	0.05	0.09	0.13	0.13	0.19	39.65	24.73	44.73	42.57	37.31	2.01	2.15	2.65	5.87
15	R 1672-1171-1-124-1	0.05	0.08	0.14	0.15	0.17	38.37	27.27	43.98	32.89	31.88	1.99	2.20	3.04	6.46
16	R 1262-1667-1-1	0.04	0.07	0.10	0.09	0.12	37.31	26.84	54.27	49.64	31.41	1.44	1.92	2.49	4.75
17	R 1860-783-1-424-1	0.05	0.07	0.09	0.14	0.16	31.62	28.57	49.25	42.86	31.34	1.55	1.87	2.34	6.98
18	RAU 1484-Aer-04	0.05	0.13	0.18	0.15	0.18	49.08	23.92	18.72	37.22	27.33	2.51	3.02	3.28	5.63
19	RCPR 8	0.06	0.09	0.14	0.15	0.17	39.02	35.15	51.29	46.67	32.62	2.36	3.22	3.63	7.59
20	CR 3631-1-3	0.06	0.08	0.15	0.11	0.14	43.21	39.73	50.35	44.25	32.51	2.33	3.20	3.81	5.60
21	CR 3632-1-2	0.04	0.10	0.15	0.11	0.12	53.92	28.68	49.96	40.26	32.41	2.34	2.87	3.28	5.73
22	CR 3634-1-3	0.06	0.08	0.09	0.11	0.13	34.27	26.66	38.95	39.86	33.16	1.95	2.24	2.48	4.23
23	CR Dhan 40	0.02	0.03	0.04	0.08	0.12	82.58	56.67	55.13	61.24	41.41	1.48	1.69	1.98	4.36
24	R-RHZ-2	0.04	0.06	0.08	0.11	0.14	32.31	33.56	33.02	35.17	33.55	1.34	2.16	2.18	3.59
25	R-RF 105	0.03	0.07	0.10	0.10	0.19	38.17	25.53	53.29	36.79	35.52	1.19	1.77	2.62	5.49
26	R 1670-3269-2-3926-1	0.05	0.09	0.12	0.11	0.20	37.26	24.62	58.35	38.07	35.73	1.69	2.30	3.15	5.55
27	R 1902-912-2-512-1	0.05	0.07	0.11	0.11	0.12	26.66	27.05	52.90	33.59	34.96	1.27	1.83	2.40	5.79
28	MTU-1010	0.03	0.09	0.11	0.08	0.16	46.02	18.87	71.83	49.25	37.16	1.45	1.77	2.03	5.69
29	R 1570-2644-2-1547-1	0.04	0.09	0.13	0.15	0.20	37.51	26.99	48.86	40.69	34.94	1.62	2.31	3.13	7.20
30	R 1432-251-103-1-1	0.05	0.11	0.13	0.13	0.16	39.26	17.92	45.25	37.28	27.70	1.76	1.91	1.84	6.02
31	CGR-547 (Bargi)	0.04	0.06	0.09	0.09	0.13	50.24	35.82	56.44	37.58	26.03	1.87	2.07	2.52	5.31
32	Digamber Dhan	0.05	0.06	0.09	0.14	0.16	42.17	37.65	38.20	39.19	29.55	2.17	2.45	2.48	3.20
33	Dadmaini Dhan	0.04	0.08	0.10	0.09	0.14	45.71	28.44	45.70	36.75	38.25	2.00	2.33	2.74	4.16
34	CR Dhan 201	0.06	0.08	0.14	0.08	0.14	27.71	27.84	53.14	41.29	36.27	1.63	2.33	2.36	4.37
35	CR Dhan 202	0.04	0.10	0.16	0.11	0.17	41.05	23.45	44.84	45.34	38.66	1.78	2.33	1.86	5.03
36	IR-64	0.05	0.07	0.13	0.09	0.15	33.99	29.42	46.14	35.47	33.26	1.79	2.15	2.54	4.16
37	Indira Barani Dhan 1	0.04	0.08	0.13	0.10	0.16	36.47	27.09	52.24	51.55	35.29	1.60	2.10	1.89	5.08
38	Sampada	0.04	0.07	0.11	0.09	0.14	14.38	16.06	44.65	31.01	33.13	0.56	1.09	1.17	3.84
	SED	0.01	0.01	0.01	0.01	0.01	5.09	4.01	2.72	4.42	1.89	0.18	0.21	0.20	0.34
	CD	0.01	0.02	0.02	0.02	0.02	10.32	8.12	5.52	8.95	3.84	0.37	0.43	0.41	0.69
	CV	11.17	9.78	9.24	8.19	5.44	13.78	14.53	12.03	9.28	5.77	9.88	9.09	7.65	6.13

0.33
0.67
5.35

Appendix (J): Mean performance of 12 quality traits of 38 rice germplasm accession under aerobic condition during wet season 2015

Sr.No.	Entry Name	H (%)	M (%)	HRR (%)	KL (mm)	KB (mm)	L:B	GS	KLAC (mm)	KBAC (mm)	L:B (AC)	ER	EI	WU (ml)
1	Indira Sona	76.80	59.44	21.52	6.8	2.2	3.1	BT	8.6	2.6	3.3	1.26	1.07	285
2	Indira Aerobic 1	73.00	61.80	40.58	4.8	2.4	2.0	SB	8.4	2.8	3.0	1.75	1.50	160
3	Swarna	74.50	64.80	44.80	5.2	2.4	2.2	SB	7.6	3.0	2.5	1.46	1.17	260
4	Basmati- 370	73.60	57.50	37.86	6.0	1.8	3.3	LS	8.8	2.7	3.3	1.47	0.98	185
5	IR-64 Drought	76.80	64.30	33.14	5.4	2.4	2.3	SB	8.6	2.6	3.3	1.59	1.47	285
6	Samleshwari	78.90	70.78	50.80	5.2	2.4	2.2	SB	9.6	2.6	3.7	1.85	1.70	160
7	Danteshwari	75.26	60.80	33.20	6.0	2.0	3.0	MS	8.8	2.4	3.7	1.47	1.22	210
8	RP 5125-2-4	79.38	72.98	40.46	6.0	2.2	2.7	MS	8.6	2.8	3.1	1.43	1.13	240
9	R 1779-321-1-112-1	74.78	58.04	33.44	6.2	2.4	2.6	LB	9.0	2.8	3.2	1.45	1.24	285
10	R 1882-306-4-243-1	76.78	54.90	31.14	5.8	2.2	2.6	MS	8.6	2.4	3.6	1.48	1.36	310
11	R 2093-1536-1-660-1	75.60	64.70	39.74	5.9	2.4	2.5	MS	8.0	2.6	3.1	1.36	1.25	160
12	IR 84887-B-15	78.80	69.70	46.48	5.6	2.4	2.3	SB	8.6	2.6	3.3	1.54	1.42	210
13	IR 83376-B-B-110-3	77.60	68.02	30.56	5.8	2.0	2.9	MS	8.0	2.6	3.1	1.38	1.06	285
14	R 1700-309-1-171-1	78.48	68.18	43.00	6.2	2.0	3.1	LS	8.8	2.4	3.7	1.42	1.18	335
15	R 1672-1171-1-124-1	80.10	63.60	32.00	5.4	2.4	2.3	SB	9.4	3.0	3.1	1.74	1.39	160
16	R 1262-1667-1-1	79.72	71.00	32.64	5.2	2.8	1.9	SB	8.8	3.0	2.9	1.69	1.58	235
17	R 1860-783-1-424-1	76.78	70.64	57.20	5.6	2.2	2.5	SB	8.0	2.5	3.2	1.43	1.26	260
18	RAU 1484-Aer-04	76.80	65.88	46.62	5.6	2.4	2.3	SB	8.4	2.6	3.2	1.50	1.38	285
19	RCPR 8	78.00	70.94	41.86	5.8	2.6	2.2	SB	8.4	2.8	3.0	1.45	1.34	210
20	CR 3631-1-3	72.36	66.68	39.32	6.2	2.4	2.6	LB	8.8	2.8	3.1	1.42	1.22	135
21	CR 3632-1-2	76.40	58.70	37.38	6.4	2.2	2.9	LB	9.0	2.7	3.3	1.41	1.15	260
22	CR 3634-1-3	69.94	59.78	36.80	6.6	2.0	3.3	LS	8.8	2.6	3.4	1.33	1.03	210
23	CR Dhan 40	76.26	67.32	41.34	5.6	2.2	2.5	SB	6.8	2.8	2.4	1.21	0.95	240
24	R-RHZ-2	75.66	64.26	36.64	5.8	2.4	2.4	SB	8.8	2.8	3.1	1.52	1.30	160
25	R-RF 105	73.44	66.80	30.52	5.8	2.2	2.6	SB	8.2	2.8	2.9	1.41	1.11	285
26	R 1670-3269-2-3926-1	77.40	67.58	43.26	6.0	2.2	2.7	MS	9.4	2.6	3.6	1.57	1.33	230
27	R 1902-912-2-512-1	77.16	60.10	35.46	6.0	2.0	3.0	MS	8.6	2.4	3.6	1.43	1.19	210
28	MTU-1010	78.40	68.00	34.70	6.0	2.0	3.0	MS	8.2	2.6	3.2	1.37	1.05	185
29	R 1570-2644-2-1547-1	74.80	66.40	41.88	5.0	2.0	2.5	SB	8.0	2.4	3.3	1.60	1.33	160
30	R 1432-251-103-1-1	73.74	63.64	37.08	5.8	2.0	2.9	MS	8.6	2.2	3.9	1.48	1.35	310
31	CGR-547 (Bargi)	75.60	63.12	29.08	5.2	2.4	2.2	SB	8.0	3.0	2.7	1.54	1.23	260
32	Digamber Dhan	75.80	69.62	41.80	5.0	2.2	2.3	SB	8.0	2.8	2.9	1.60	1.26	335

Appendix (J) continued...

33	Dadhmaini Dhan	76.20	67.44	32.64	5.0	2.2	2.3	SB	8.6	2.6	3.3	1.72	1.46	340
34	CR Dhan 201	75.56	70.06	35.38	6.2	2.0	3.1	LS	9.2	2.8	3.3	1.48	1.06	235
35	CR Dhan 202	75.14	66.58	34.52	5.4	2.2	2.5	SB	8.8	2.4	3.7	1.63	1.49	285
36	IR-64	76.60	62.40	27.88	6.2	2.4	2.6	LB	8.4	2.6	3.2	1.35	1.25	285
37	Indira Barani Dhan 1	68.70	62.60	27.24	5.6	2.2	2.5	SB	8.0	2.8	2.9	1.43	1.12	335
38	Sampada	70.80	62.40	45.00	5.2	2.2	2.4	SB	7.8	2.8	2.8	1.50	1.18	210
	Mean	75.83	65.04	37.50	5.72	2.24	2.59	-	8.50	2.67	3.21	1.49	1.26	241.84
	Min	68.70	54.90	21.52	4.80	1.80	1.86	-	6.80	2.20	2.43	1.21	0.95	135.00
	Max	80.10	72.98	57.20	6.80	2.80	3.33	-	9.60	3.00	3.91	1.85	1.70	340.00
	SE	0.29	0.54	1.14	0.19	0.13	0.22	-	0.18	0.11	0.18	0.11	0.15	3.74
	SD	2.58	4.38	7.01	0.47	0.20	0.36	-	0.54	0.19	0.33	0.13	0.17	58.26

H- Hulling percent; **M**-Milling percent; **HRR**-Head Rice Recovery percent; **KL**-Kernel length; **KB**-Kernel breadth; **L:B**-Length:Breadth ratio; **GS**- Grain shape; **KLAC**-Kernel length after cooking; **KBAC**-Kernel breadth after cooking; **L:B (AC)**-Length:Breadth ratio after cooking; **ER**-Elongation ratio; **EI**-Elongation index; **WU**-Water uptake; **SB**-Short Bold; **MS**- Medium Slender; **LS**- Long Slender; **LB**- Long Bold; **BT**- Basmati type.

Appendix (K): Mean performance of 12 quality traits of 38 rice germplasm accession under anaerobic condition during wet season 2015

Sr. No.	Entry Name	H (%)	M (%)	HRR (%)	KL (mm)	KB (mm)	L:B	GS	KLAC (mm)	KBAC (mm)	L:B (AC)	ER	EI	WU (ml)
1	Indira Sona	74.60	59.14	36.46	7.0	2.0	3.5	BT	9.3	2.8	3.3	1.33	0.95	290
2	Indira Aerobic 1	77.70	62.16	41.12	5.2	2.2	2.4	SB	8.8	3.0	2.9	1.69	1.24	160
3	Swarna	78.50	68.24	53.68	5.2	2.2	2.4	SB	8.0	3.4	2.4	1.54	1.00	210
4	Basmati- 370	75.48	61.70	43.00	6.2	2.0	3.1	LS	8.6	3.2	2.7	1.39	0.87	235
5	IR-64 Drought	75.60	65.00	45.20	5.8	2.2	2.6	MS	8.6	3.0	2.9	1.48	1.09	260
6	Samleshwari	73.68	62.30	53.08	5.8	2.2	2.6	MS	9.8	2.8	3.5	1.69	1.33	185
7	Danteshwari	70.44	66.44	44.04	6.2	2.0	3.1	LS	8.8	3.2	2.8	1.42	0.89	210
8	RP 5125-2-4	72.08	56.80	44.70	6.0	2.2	2.7	MS	9.6	3.2	3.0	1.60	1.10	200
9	R 1779-321-1-112-1	72.94	60.68	39.38	6.0	2.0	3.0	MS	9.4	3.1	3.0	1.57	1.01	260
10	R 1882-306-4-243-1	70.16	54.68	34.36	5.8	2.2	2.6	MS	8.6	3.0	2.9	1.48	1.09	285
11	R 2093-1536-1-660-1	73.60	59.88	40.72	6.4	2.2	2.9	LB	8.4	3.4	2.5	1.31	0.85	185
12	IR 84887-B-15	75.60	59.30	49.00	5.6	2.4	2.3	SB	8.6	2.8	3.1	1.54	1.32	185
13	IR 83376-B-B-110-3	79.22	65.08	52.36	6.0	2.0	3.0	MS	7.8	3.0	2.6	1.30	0.87	300
14	R 1700-309-1-171-1	76.40	62.40	55.98	5.8	2.0	2.9	MS	9.0	3.0	3.0	1.55	1.03	310
15	R 1672-1171-1-124-1	74.36	55.78	45.48	5.4	2.2	2.5	SB	9.4	3.0	3.1	1.74	1.28	180
16	R 1262-1667-1-1	75.00	64.32	55.64	5.4	2.4	2.3	SB	9.0	2.8	3.2	1.67	1.43	235
17	R 1860-783-1-424-1	69.80	60.00	50.54	5.6	2.2	2.5	SB	8.8	3.0	2.9	1.57	1.15	260
18	RAU 1484-Aer-04	74.42	68.00	54.16	5.6	2.4	2.3	SB	9.0	2.8	3.2	1.61	1.38	200
19	RCPR 8	77.30	63.60	53.40	5.6	2.6	2.2	SB	8.6	3.2	2.7	1.54	1.25	160
20	CR 3631-1-3	79.22	65.08	54.56	6.0	2.4	2.5	MS	8.8	3.0	2.9	1.47	1.17	110
21	CR 3632-1-2	77.12	63.04	40.46	6.4	2.2	2.9	LB	9.2	3.2	2.9	1.44	0.99	210
22	CR 3634-1-3	76.40	58.80	42.48	6.0	2.0	3.0	MS	8.8	2.8	3.1	1.47	1.05	210
23	CR Dhan 40	73.20	60.88	41.10	5.4	2.2	2.5	SB	7.0	3.0	2.3	1.30	0.95	235
24	R-RHZ-2	74.20	61.56	48.92	5.8	2.2	2.6	MS	9.2	3.0	3.1	1.59	1.16	160
25	R-RF 105	72.06	59.00	33.12	5.8	2.4	2.4	SB	8.6	3.2	2.7	1.48	1.11	270
26	R 1670-3269-2-3926-1	74.60	62.02	45.52	6.0	2.2	2.7	MS	9.8	3.0	3.3	1.63	1.20	260
27	R 1902-912-2-512-1	75.60	55.16	39.88	6.0	2.0	3.0	MS	8.8	2.7	3.3	1.47	1.09	235
28	MTU-1010	71.22	57.02	46.72	5.8	2.0	2.9	MS	8.8	3.2	2.8	1.52	0.95	210
29	R 1570-2644-2-1547-1	76.72	69.78	56.38	5.2	2.2	2.4	SB	7.8	2.8	2.8	1.50	1.18	160
30	R 1432-251-103-1-1	78.10	67.70	44.10	6.0	2.0	3.0	MS	8.6	2.6	3.3	1.43	1.10	300
31	CGR-547 (Bargi)	76.86	50.58	33.30	5.4	2.4	2.3	SB	8.4	3.6	2.3	1.56	1.04	260
32	Digamber Dhan	73.20	64.80	54.84	5.2	2.2	2.4	SB	8.2	3.2	2.6	1.58	1.08	310

Appendix (K) continued...														
33	Dadhmaini Dhan	75.00	62.90	55.28	5.2	2.2	2.4	SB	9.0	3.2	2.8	1.73	1.19	320
34	CR Dhan 201	75.26	63.28	44.08	6.0	2.0	3.0	MS	9.4	3.2	2.9	1.57	0.98	295
35	CR Dhan 202	72.54	66.60	50.46	5.8	2.4	2.4	SB	9.2	3.0	3.1	1.59	1.27	260
36	IR-64	75.60	65.20	45.12	6.0	2.0	3.0	MS	8.6	2.9	3.0	1.43	0.99	285
37	Indira Barani Dhan 1	67.22	59.00	47.20	6.0	2.2	2.7	MS	8.4	3.2	2.6	1.40	0.96	310
38	Sampada	73.26	60.24	46.16	5.4	2.2	2.5	MS	8.2	3.0	2.7	1.52	1.11	235
	Mean	74.59	61.79	46.37	5.79	2.18	2.67	-	8.76	3.04	2.90	1.52	1.10	235.39
	Min	67.22	50.58	33.12	5.20	2.00	2.15	-	7.00	2.60	2.33	1.30	0.85	110.00
	Range	79.22	69.78	56.38	7.00	2.60	3.50	-	9.80	3.60	3.50	1.74	1.43	320.00
	SE	0.31	0.53	0.97	0.16	0.10	0.18	-	0.19	0.12	0.16	0.09	0.14	3.44
	SD	2.69	4.17	6.66	0.39	0.16	0.32	-	0.57	0.21	0.29	0.11	0.15	52.86

H- Hulling percent; **M**-Milling percent; **HRR**-Head Rice Recovery percent; **KL**-Kernel length; **KB**-Kernel breadth; **L:B**-Length:Breadth ratio; **GS**- Grain shape; **KLAC**-Kernel length after cooking; **KBAC**-Kernel breadth after cooking; **L:B (AC)**-Length:Breadth ratio after cooking; **ER**-Elongation ratio; **EI**-Elongation index; **WU**-Water uptake; **SB**-Short Bold; **MS**- Medium Slender; **LS**- Long Slender; **LB**- Long Bold; **BT**- Basmati type.

Appendix (L): Fe and Zn Content in brown rice from selected 38 rice germplasm accessions over different N regimes under variable environments.

Sr. No.	Entry Name	Fe mg/kg (ppm)						Zn mg/kg (ppm)					
		N ⁰			NH ₄ ⁺			N ⁰			NH ₄ ⁺		
		Aerobic	Anaerobic	Aerobic	Anaerobic	NO ₃ ⁻	Aerobic	Anaerobic	Aerobic	Anaerobic	NO ₃ ⁻	Aerobic	Anaerobic
1	Indira Sona	7.2	9.4	12.2	8.9	8.1	11.2	12.3	19.9	16.0	13.8	21.4	
2	Indira Aerobic 1	7.0	9.0	7.2	8.6	9.8	9.2	6.8	18.7	6.9	17.0	14.8	
3	Swarna	7.3	8.4	7.7	9.5	7.8	9.7	15.9	16.3	16.2	17.0	18.1	
4	Basmati- 370	9.6	11.4	16.2	12.7	12.7	13.7	16.7	22.7	11.0	22.7	24.9	
5	IR-64 Drought	7.8	8.5	15.9	11.3	16.5	10.0	9.9	18.7	9.2	18.0	20.2	
6	Samleshwari	7.8	7.6	10.0	9.9	13.9	9.1	11.5	16.4	9.3	17.4	19.4	
7	Danteshwari	9.9	10.3	11.7	13.2	20.8	12.3	12.3	21.7	12.5	19.4	20.9	
8	RP 5125-2-4	11.0	10.0	11.3	11.1	12.7	11.2	17.3	18.9	11.0	18.1	20.0	
9	R 1779-321-1-112-1	8.2	9.5	11.1	9.9	12.3	13.5	15.3	19.0	9.8	19.1	20.6	
10	R 1882-306-4-243-1	8.7	10.9	10.0	9.7	13.1	12.6	15.5	20.0	10.5	18.6	20.3	
11	R 2093-1536-1-660-1	10.3	9.2	12.7	11.1	16.1	12.2	19.0	19.8	14.6	19.4	22.4	
12	IR 84887-B-15	11.4	8.1	9.7	9.6	12.3	11.5	16.8	20.5	12.5	21.7	21.1	
13	IR 83376-B-B-110-3	9.8	8.8	9.1	10.2	11.2	9.8	15.2	23.3	9.4	20.4	22.9	
14	R 1700-309-1-171-1	6.9	9.8	9.7	10.0	10.0	10.0	11.8	15.5	10.7	17.9	21.7	
15	R 1672-1171-1-124-1	9.2	8.1	10.8	8.7	10.3	10.3	9.2	16.8	10.0	19.0	17.9	
16	R 1262-1667-1-1	9.2	11.0	12.6	9.6	11.0	10.7	16.5	19.5	14.9	19.7	20.5	
17	R 1860-783-1-424-1	9.4	10.1	10.0	9.4	10.9	9.9	16.1	18.9	14.5	19.1	21.7	
18	RAU 1484-Aer-04	12.3	10.7	12.6	11.2	13.2	10.8	20.6	21.3	10.9	23.4	23.5	
19	RCPR 8	10.8	9.4	10.7	12.1	12.4	10.8	19.0	19.7	12.3	23.2	20.4	
20	CR 3631-1-3	11.0	10.4	12.5	12.0	12.7	12.9	14.4	24.3	8.9	23.6	23.3	
21	CR 3632-1-2	8.4	9.4	9.2	9.2	11.3	10.8	9.9	19.5	7.0	17.4	19.3	
22	CR 3634-1-3	8.7	9.7	13.4	10.6	10.3	9.1	12.4	20.6	10.7	19.0	18.1	
23	CR Dhan 40	9.8	9.3	10.6	12.2	11.7	12.3	20.1	25.6	21.0	25.5	21.4	
24	R-RHZ-2	9.8	10.5	10.8	11.8	10.9	11.2	16.0	19.0	14.6	19.5	19.8	
25	R-RF 105	10.4	11.5	9.9	11.1	10.4	10.1	14.8	22.6	10.9	20.3	19.5	
26	R 1670-3269-2-3926-1	9.8	12.8	8.0	10.0	10.1	12.3	12.0	17.5	8.9	17.5	25.7	
27	R 1902-912-2-512-1	9.0	12.1	8.8	10.1	11.9	11.4	15.8	20.4	9.9	19.6	23.2	
28	MTU-1010	7.1	8.1	8.7	10.2	7.1	9.9	10.5	16.8	8.5	18.5	18.0	
29	R 1570-2644-2-1547-1	6.9	10.2	6.7	8.1	7.8	10.3	6.7	19.1	6.3	14.7	18.4	
30	R 1432-251-103-1-1	8.9	9.1	8.0	9.5	8.9	8.9	13.2	20.0	12.6	17.2	19.0	
31	CGR-547 (Bargi)	8.2	10.0	12.1	11.2	13.5	12.9	17.8	22.5	21.4	23.1	22.1	
32	Digamber Dhan	8.6	8.4	9.4	7.8	9.1	9.6	13.1	16.9	12.6	17.0	17.7	
33	Dadhmairi Dhan	9.7	10.1	8.6	8.6	9.1	9.7	13.2	20.1	11.8	18.0	19.2	
34	CR Dhan 201	10.2	8.4	7.5	9.1	11.3	11.7	11.8	20.1	9.5	23.2	22.9	
35	CR Dhan 202	9.9	7.9	11.4	9.3	9.5	10.8	14.8	19.1	13.6	22.0	22.5	
36	IR-64	9.0	7.9	8.7	9.4	8.6	10.6	8.8	17.9	10.9	19.0	21.4	
37	Indira Barani Dhan 1	9.0	9.8	10.6	11.4	10.8	10.4	20.2	19.6	19.3	20.3	19.2	
38	Sampada	7.5	8.5	7.9	10.4	7.8	12.4	13.5	14.0	14.2	14.8	15.5	
Mean		9.1	9.6	10.4	10.2	11.3	10.9	14.1	19.5	11.9	19.4	20.5	
Min		6.9	7.6	6.7	7.8	7.1	8.9	6.7	14.0	6.3	14.7	14.8	
Max		12.3	12.8	16.2	13.2	20.8	13.7	20.6	25.6	21.4	25.5	25.7	
SD		1.4	1.2	2.2	1.3	2.7	1.3	3.6	2.5	3.5	2.5	2.3	

RESUME

Name : Ambhure Ram Ganpatrao
Date of birth : 5th Oct 1987
Present Address : Room No. 217, Sundaram Boys Hostel, IGKV, Jora
Raipur (Chhattishgarh) 492012
Phones : 9860999168 and 8827083808
E. mail : ambhure.ram05@gmail.com
Permanent address : At. Post. Chandaj
Tq. Jinture
Dist. Parbhani (431 508) Maharashtra.

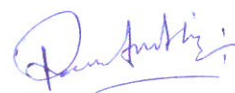
Academic Qualification

Degree	Year	University
B. Sc. (Ag.)	2006-2010	Vasantrao Naik Marathwada Krishi Vidyapeeth Parbhani
M. Sc. (Ag.)	2010-2012	Vasantrao Naik Marathwada Krishi Vidyapeeth Parbhani
Ph. D.	2014- Contd...	Indira Gandhi Krishi Vishwavidyalaya, Raipur

Work Experience:

1. Actively participation in NSS camp during year 2008.
2. Successfully Completed Rural Agricultural Work Experience (RAWE) for six month at Najikpangari Tq. Badnapur Dist. Jalna.
3. Successfully arranged of Shetkari melava and Vaccination programme during RAWE in 2009-10.
4. Worked as Plant Breeder in R and D division for Nirmal Seeds Pvt. Ltd., Bhadgaon Tq. Pachora Dist. Jalgaon from the period 8 Jan, 2013 to 30 Sep, 2014.

Publications : 4


Signature